

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 16, 2002, 17:27:03 ; Search time 33.873 Seconds
(without alignments)
1526.325 Million cell updates/sec

Title: US-09-596-196-4

Perfect score: 2104
Sequence: 1 MMSPSQASLFLNVCIFICG.....PVKIKSVSMKIRRMYPYRK 388

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: A_Geneseq_101002:*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2104	100.0	388	22	Human prothrombina
2	2100	99.8	388	22	Human angiotensin
3	2086	99.1	388	23	Human polypeptide
4	2000	95.1	368	22	Human prothrombina
5	1729	82.2	326	22	Human novel protei
6	1729	82.2	326	22	Human novel protei
7	1729	82.2	326	22	Human prothrombina
8	1711.5	81.3	335	23	Human MDPF SEQ ID
9	1625	77.2	306	22	Human prothrombina
10	1299	61.7	237	22	Human prothrombina

11	1265	60.1	240	22	Human prothrombina
12	634	30.1	141	22	Novel human diagno
13	628.5	29.9	138	22	Novel human diagno
14	521	24.8	116	22	Novel human diagno
15	425	20.2	491	20	Human zapot protei
16	425	20.2	491	20	Human TIE ligand N
17	425	20.2	491	21	Angiotensin-like
18	425	20.2	491	21	Human PRO188 prote
19	425	20.2	491	21	Amino acid sequenc
20	425	20.2	491	21	An angiotensin-re
21	425	20.2	491	22	Human FRO188 polyp
22	425	20.2	491	22	Human neovasculari
23	425	20.2	491	22	Human angiogenesis
24	425	20.2	491	23	Human TIE ligand N
25	421	20.0	491	23	Human secreted pro
26	420	20.0	491	21	Protein encoded by
27	414	19.7	439	20	Human polypeptide
28	413.5	19.7	439	20	Human prothrombina
29	405.5	19.3	432	20	Mouse prothrombina
30	403.5	19.2	497	17	Human TIE-2 ligand
31	403.5	19.2	497	17	Human TIE-2 ligand
32	403.5	19.1	497	19	Amino acid sequenc
33	401.5	19.1	360	21	Mouse angiotensin
34	400.5	19.0	493	21	Human ORFX ORF1476
35	400	19.0	386	20	Human normal uteru
36	400	19.0	493	20	Human TIE ligand N
37	400	19.0	493	21	Angiotensin-like
38	400	19.0	493	21	PSBO-3 protein enc
39	400	19.0	493	21	Human scarface 1 p
40	400	19.0	493	22	Human PRO196 polyp
41	400	19.0	493	22	Amino acid sequenc
42	400	19.0	493	22	Human 410 angioten
43	400	19.0	493	23	Human angiotensin
44	400	19.0	493	22	Human matrix-remod
45	400	19.0	493	23	Human TIE ligand N

ALIGNMENTS

RESULT 1	AA82584	
ID	AA82584 standard; Protein; 388 AA.	
XX	AA82584;	
AC		
XX	02-OCT-2001 (first entry)	
XX		
DE	Human prothrombinase-like polypeptide.	
XX		
KW	Prothrombinase-like polypeptide; human; haemostatic; cardiant;	
KW	nephrotropic; antidiabetic; hepatotropic; antiviral; cytostatic;	
KW	antidiabetic; antidiabetic; antidiabetic; osteoporosis;	
KW	immunomodulatory; antirheumatic; antidiabetic; antidiabetic;	
XX	thrombolytic; diagnosis; therapy.	
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..20
FT	Protein	/label= Signal_peptide
FT		21..388
FT		/label= Mature.protein
FT	Domain	/note= "separately claimed in Claim 10"
FT		181..217
FT		/note= "fibrinogen beta/gamma chain"
FT		/note= "separately claimed in Claim 10"
FT		222..234
FT		/note= "fibrinogen beta/gamma chain"
FT		/note= "separately claimed in Claim 10"
FT		271..285
FT		/note= "fibrinogen beta/gamma chain"
FT		/note= "separately claimed in Claim 10"

FT	Domain		324...353	
ET	/note= "fibrinogen beta/gamma chain"			
FX	/note= "separately claimed in Claim 10"			
PX				
PN	WO200153456-A2.			
XX				
PD	26-JUL-2001.			
XX				
PF	22-DEC-2000; 2000WO-US35061.			
XX				
PR	21-JAN-2000; 2000US-0488725.			
PR	25-JAN-2000; 2000US-0491404.			
PR	25-APR-2000; 2000US-0552317.			
PR	17-JUN-2000; 2000US-0596196.			
XX	31-AUG-2000; 2000US-0643313.			
PA	(HYSE-) HYSEQ INC.			
PI	Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;			
PI	Arterburn MC, Tang YT, Liu C, Drmanac R;			
DR	WPI; 2001-483140/52.			
XX	N-PSDB; AAH26235, AAH26236.			
PT	Novel prothrombinase-like polypeptides and polynucleotides useful in			
XX	diagnosing and treating e.g. myocardial infarction and diabetes -			
PS	Claim 10; Page 126-127; 140pp; English.			
CC	The present sequence is that of a novel human secreted			
CC	prothrombinase-like polypeptide (PLP). The polypeptide has a			
CC	predicted mol.wt. of 43,000 (unglycosylated) and shows amino acid			
CC	sequence similarity to human prothrombinase Fg12 protein. The			
CC	sequence was predicted from polynucleotides (see AAH26235-36)			
CC	derived from a human ovary cDNA clone. PLP polynucleotides and			
CC	polypeptides, including the mature protein, polypeptides including			
CC	PLP fibrinogen chains, and a soluble splice variant (see AAH82590),			
CC	can be used in the diagnosis, treatment and/or prevention of diseases			
CC	associated with the dysregulation of coagulation pathways, such as			
CC	haemophilia, myocardial infarction, glomerular disease, diabetes,			
CC	fulminant viral hepatitis and atherosclerosis. They may also be			
CC	beneficial in the treatment of viral infections and some forms of			
CC	cancer. A claimed method of treating a subject in need of enhanced			
CC	PLP activity or expression involves the administration of PLP, a			
CC	PLP agonist or a polynucleotide encoding PLP. A claimed method of			
CC	treating a subject having need to inhibit activity or expression of			
CC	PLP involves the administration of a PLP antagonist, a			
CC	polynucleotide that inhibits expression of a PLP polynucleotide,			
CC	or a polypeptide that competes with the PLP for its ligand. The			
CC	polypeptides can also be used to raise antibodies, as food			
CC	supplements, and to screen for agonists and antagonists.			
SQ	Sequence 388 AA;			
Query Match	100.0%; Score 2104; DB 22; Length 388;			
Best Local Similarity	100.0%; Pred. No. 8.6e-205;			
Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
OY	1 MMSPQASLLFNVCIFGCEVYGNCVCHSHSDSSVNVIVEGGSNAKESKNDFVCKED 60			
DB	1 MMSPQASLLFNVCIFGCEVYGNCVCHSHSDSSVNVIVEDGSNAKESKNDPVCKED 60			
OY	61 CEESCDVKTKITREKHCFRCMLQNSIYSYSTSKKLRLNMMDDEOQASLDYLSNOVNELM 120			
DB	61 CEESCDVKTKITREKHCFRCMLQNSIYSYSTSKKLRLNMMDDEOQASLDYLSNOVNELM 120			
OY	121 NRVLLTTEVFKKOLDPPRHVPVOSHGLDCTDKTTIGSVTKTPSGGLVIHPHGSSYPPE 180			
DB	121 NRVLLTTEVFKKOLDPPRHVPVOSHGLDCTDKTTIGSVTKTPSGGLVIHPHGSSYPPE 180			
OY	181 VWCDDVDYGGCGVTVOIKRIDGITIDFQRIMCVDLDSFGDLGGEFWLGKIKFIYNOKMTS 240			
DB	181 VWCDDVDYGGCGVTVOIKRIDGITIDFQRIMCVDLDSFGDLGGEFWLGKIKFIYNOKMTS 240			

Oy	241	FMVAALAESEDDTLAAVSYDNFMLEDDTRFRKHHILGRYSGNMGDAFRGLAKKEDNONAMPE	300		
Db	241	FMVAALAESEDDTLAAVSYDNFMLEDDTRFRKHHILGRYSGNMGDAFRGLAKKEDNONAMPE	300		
Oy	301	STSDVDNDCGRPACTLVAGOSVKSCHLHNKTGMWFNECGLANLNGIHHSGLKLTATGIOM	360		
Db	301	STSDVDNDCGRPACTLVAGOSVKSCHLHNKTGMWFNECGLANLNGIHHSGLKLTATGIOM	360		
Oy	361	GTWTKNNSPVAKIKSVSKIRRMATPYRK	388		
Db	361	GTWTKNNSPVAKIKSVSKIRRMATPYRK	388		
RESULT 2					
ID	AAV72622	AAV72622 standard; Protein; 388 AA.			
AC	AAV72622;				
XX	02-MAY-2001	(first entry)			
DE	Human angiotensinogen protein, CG144.				
XX					
KW	Human; angiotensin; angiogenesis; gene therapy; CG144;				
KW	vascular stability; neovascularisation; nutritional supplement; therapy;				
KW	myocardial infarction; proliferative retinopathy; atherosclerosis;				
KW	coronary heart disease; arterial ischaemia; bone disorder; cancer;				
KW	abnormal vascular growth; anaemia; chronic inflammation; immune disorder;				
KW	haematopoiesis related disorder; coagulation disorder; leukaemia;				
KW	cytosolic; vasotropic; food supplement; nervous system disorder;				
XX	drug screening.				
OS	Homo sapiens.				
XX					
FT	Key	Location/Qualifiers			
FT	Peptide	1..22			
FT	Protein	/label= Signal_peptide			
FT	Domain	23..388			
FT	Domain	/note="Mature angiotensinogen protein, CG144"			
FT	Domain	193..230			
FT	Domain	/note="Fibrinogen domain"			
FT	Domain	234..247			
FT	Domain	/note="Fibrinogen domain"			
FT	Domain	283..301			
FT	Domain	/note="Fibrinogen domain"			
FT	Domain	307..321			
FT	Domain	/note="Fibrinogen domain"			
FT	Domain	337..366			
FT	Domain	/note="Fibrinogen domain"			
XX					
PN	WO200105825-A2.				
XX					
PD	25-JAN-2001.				
XX					
PF	17-JUL-2000; 2000WO-US19429.				
XX					
PR	16-JUL-1999; 99US-0354881.				
XX					
PA	(HYSE-) HYSEQ INC.				
XX					
PI	Ballinger DG, Montgomery JR;				
XX					
DR	WPI: 2001-091966/10.				
XX					
DR	N-PSDB: AADD02607.				
XX					
PT	Human angiotensinogen proteins and DNA encoding sequences useful for				
XX	preventing, treating or ameliorating a medical condition in a mammalian				
XX	subject e.g. arthritis and cancer -				
XX					
ES	Claim 10; Page 111-112; 132pp; English.				
XX					
CC	The present sequence is human angiotensinogen protein, CG144.				

CC The present invention relates to human angiotensin polypeptides such
 CC as CG006, CG007, CG015, CG144 and CG250. The angiotensin polypeptides
 CC are used as hybridisation probes, for chromosome and gene mapping, to
 CC identify polymorphism and for recombinant protein production.
 CC Angiotensin may be useful for modulating vascular stability and
 CC neovascularisation associated with various pathologies. It is used as a
 CC nutritional supplement, molecular weight marker and in gene therapy. It
 CC is also used for preventing, treating or ameliorating angiogenesis
 CC related disorders such as myocardial infarction, proliferative
 CC retinopathy, atherosclerosis, coronary heart disease, arterial
 CC bone disorders (e.g., osteoporosis), abnormal vascular growth, cancer,
 CC anaemia and chronic inflammatory reactions (e.g., asthma and arthritis) and immune
 CC disorders (e.g., inflammatory diseases and autoimmune diseases),
 CC haematopoiesis related disorders (e.g., myeloid or lymphoid cell
 CC deficiencies), coagulation disorders, leukaemias and nervous system
 CC disorders. It is also used in drug screening techniques for screening
 CC compounds which are able to modulate the expression or activity of
 CC angiotensin. The compounds can also be used to treat diseases and
 CC disorders.

XX Sequence 388 AA;

Query Match 99.8%; Score 2100; DB 22; Length 388;

Best Local Similarity 99.7%; Pred. No. 2.2e-204; Mismatches 1; Indels 0; Gaps 0;

Matches 387; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MMSPSQASLFLNVCIFGCEVQNCVHSTDSVNIIVEDGSNAKDESKNDTVCKED 60
 DB 1 MMSPSQASLFLNVCIFGCEVQNCVHSTDSVNIIVEDGSNAKDESKNDTVCKED 60

QY 61 CEESCDVTKITREKHKMCRNLQNSIVSYSTRSKLLRNMMDEQASLDYLSNOVNELM 120
 DB 61 CEESCDVTKITREKHKMCRNLQNSIVSYSTRSKLLRNMMDEQASLDYLSNOVNELM 120

QY 121 NRVLTLTEVFRKQDPPRPHRVQSHGDCDIDKDTIGSVTKTPSGLYIIHPEGSSYPFE 180
 DB 121 NRVLTLTEVFRKQDPPRPHRVQSHGDCDIDKDTIGSVTKTPSGLYIIHPEGSSYPFE 180

QY 181 VMCDMDYRGSGMTYQKRIIDGIDFQRLMCDYLDGFGDLGFEFWGLKRIFYIYQNKMTS 240
 DB 181 VMCDMDYRGSGMTYQKRIIDGIDFQRLMCDYLDGFGDLGFEFWGLKRIFYIYQNKMTS 240

QY 241 FMLVVALESEDDTLAYASYDNFWLEDETRFRKMHGGRYSNGADAFRLKKEDNONAMPF 300
 DB 241 FMLVVALESEDDTLAYASYDNFWLEDETRFRKMHGGRYSNGADAFRLKKEDNONAMPF 300

QY 301 STSDVDNDGCRPACLVNGQSVKSCSHLNKTGMWNECGLANLNGIHFSGLATGIGIOW 360
 DB 301 STSDVDNDGCRPACLVNGQSVKSCSHLNKTGMWNECGLANLNGIHFSGLATGIGIOW 360

QY 361 GTWTKNNSPVKIKSVSMKIRRMYNPYFK 388
 DB 361 GTWTKNNSPVKIKSVSMKIRRMYNPYFK 388

RESULT 3
 ABB77546
 ID ABB77546 standard; Protein; 388 AA.

XX ABB77546;

XX 05-AUG-2002 (first entry)

XX Human polypeptide SEQ ID NO 2.

XX Human; collagen II; aggrecan; antiarthritic; cartilage;

XX arthritis deformans.

XX Homo sapiens.

XX MO30242448-A1.
 XX 30-MAY-2002.

XX 21-NOV-2001; 2001WO-JP10150.
 XX
 XX 22-NOV-2000; 2000JP-0356378.
 XX
 XX (YAMA) YAMANOUCHI PHARM CO LTD.
 XX
 XX Yasunaga K;
 XX
 XX WPI: 2002-463631/49.
 XX
 XX N-PSDB: ABL60374.

XX Human polypeptide promoting collagen II and aggrecan production for
 XX treatment and prevention of arthritis deformans -

XX Claim 1; Page 56-57; 72pp; Japanese.

XX The invention relates to human polypeptide (ABB77546) promoting collagen
 XX II and/or aggrecan activity created by addition, deletion and/or
 XX substitution. The polypeptide has antiarthritic activity and promotes
 XX collagen II and aggrecan production in cartilage cells. It is useful for
 XX treatment and prevention of arthritis deformans.

XX Sequence 388 AA;

Query Match 99.1%; Score 2086; DB 23; Length 388;

Best Local Similarity 99.5%; Pred. No. 5.8e-203; Mismatches 2; Indels 0; Gaps 0;

QY 1 MMSPSQASLFLNVCIFGCEVQNCVHSTDSVNIIVEDGSNAKDESKNDTVCKED 60
 DB 1 MMSPSQASLFLNVCIFGCEVQNCVHSTDSVNIIVEDGSNAKDESKNDTVCKED 60

QY 61 CEESCDVTKITREKHKMCRNLQNSIVSYSTRSKLLRNMMDEQASLDYLSNOVNELM 120
 DB 61 CEESCDVTKITREKHKMCRNLQNSIVSYSTRSKLLRNMMDEQASLDYLSNOVNELM 120

QY 121 NRVLTLTEVFRKQDPPRPHRVQSHGDCDIDKDTIGSVTKTPSGLYIIHPEGSSYPFE 180
 DB 121 NRVLTLTEVFRKQDPPRPHRVQSHGDCDIDKDTIGSVTKTPSGLYIIHPEGSSYPFE 180

QY 181 VMCDMDYRGSGMTYQKRIIDGIDFQRLMCDYLDGFGDLGFEFWGLKRIFYIYQNKMTS 240
 DB 181 VMCDMDYRGSGMTYQKRIIDGIDFQRLMCDYLDGFGDLGFEFWGLKRIFYIYQNKMTS 240

QY 241 FMLVVALESEDDTLAYASYDNFWLEDETRFRKMHGGRYSNGADAFRLKKEDNONAMPF 300
 DB 241 FMLVVALESEDDTLAYASYDNFWLEDETRFRKMHGGRYSNGADAFRLKKEDNONAMPF 300

QY 301 STSDVDNDGCRPACLVNGQSVKSCSHLNKTGMWNECGLANLNGIHFSGLATGIGIOW 360
 DB 301 STSDVDNDGCRPACLVNGQSVKSCSHLNKTGMWNECGLANLNGIHFSGLATGIGIOW 360

QY 361 GTWTKNNSPVKIKSVSMKIRRMYNPYFK 388
 DB 361 GTWTKNNSPVKIKSVSMKIRRMYNPYFK 388

RESULT 4
 AAB82589
 ID AAB82589 standard; Protein; 368 AA.

XX AAB82589;

XX 02-OCT-2001 (first entry)

XX Human prothrombinase-like polypeptide (mature protein).

XX Prothrombinase-like polypeptide; human; haemostatic; cardiac;
 XX nephrotropic; antidiabetic; hepatotropic; antiviral; cystostatic;
 XX antiarteriosclerotic; antilicer; vulnery; osteoporosis;
 XX immunomodulatory; antineumatic; antiarthritic; antiinflammatory;
 XX thrombolytic; diagnosis; therapy.

```

XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 161..197
XX /note= "fibrinogen beta/gamma chain"
XX Domain 202..214
XX /note= "fibrinogen beta/gamma chain"
XX Domain 251..265
XX /note= "fibrinogen beta/gamma chain"
XX Domain 304..333
XX /note= "fibrinogen beta/gamma chain"
XX
XX WO200153456-A2.
XX
XX 26-JUL-2001.
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XX 22-DEC-2000; 2000WO-US35061.
XX
XX 21-JAN-2000; 2000US-0488725.
XX 25-JAN-2000; 2000US-0491404.
XX 25-APR-2000; 2000US-0552317.
XX 17-JUN-2000; 2000US-0596196.
XX 31-AUG-2000; 2000US-0643313.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
XX Arterburn MC, Tang YT, Liu C, Drmanac R;
XX
XX WPI: 2001-483140/52.
XX N-PSDB: AAH26235, AAH26236.
XX
XX Novel prothrombinase-like polypeptides and polynucleotides useful in
XX diagnosing and treating e.g. myocardial infarction and diabetes -
XX
XX Claim 10; Page 128-129; 140pp; English.
XX
XX The present sequence is that of human secreted prothrombinase-like
XX polypeptide (PLP) mature polypeptide, as predicted from
XX polynucleotides (see AAH26235-36) derived from an ovary cDNA clone.
XX PLP polynucleotides and polypeptides, including the mature protein,
XX can be used in the diagnosis, treatment and/or prevention of diseases
XX associated with the dysregulation of coagulation pathways, such as
XX haemophilia, myocardial infarction, glomerular disease, diabetes,
XX fulminant viral hepatitis and atherosclerosis. They may also be
XX beneficial in the treatment of viral infections and some forms of
XX cancer. A claimed method of treating a subject in need of enhanced
XX PLP activity or expression involves the administration of PLP, a
XX PLP agonist or a polynucleotide encoding PLP. A claimed method of
XX treating a subject having need to inhibit activity or expression of
XX PLP involves the administration of a PLP antagonist, a
XX polynucleotide that inhibits expression of a PLP polynucleotide,
XX or a polypeptide that competes with the PLP for its ligand. The
XX polypeptides can also be used to raise antibodies, as food
XX supplements, and to screen for agonists and antagonists.
XX
XX Sequence 368 AA:
XX
XX Query Match 95.1%; Score 2000; DB 22; Length 368;
XX Best Local Similarity 100.0%; Pred. No. 2,9e-144;
XX Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 21 EVVQNCVHSTDSVVNIVEDGSKNDYCKEDCESCDVTKITREKHFMC 80
XX |||||||
XX 1 EVVQNCVHSTDSVVNIVEDGSKNDYCKEDCESCDVTKITREKHFMC 60
XX
XX 81 RMLQNSIVSYSTKTKLLNNMDEQOASLDYLSNOVNEMLNRYLLTTEYFKQDLPFH 140
XX |||||||
XX 61 RMLQNSIVSYSTKTKLLNNMDEQOASLDYLSNOVNEMLNRYLLTTEYFKQDLPFH 120
XX
XX 141 RVQSHGLDCTDIKDTIGSVTKTPSGLYTIHPGSSYPEFVCMQMDYRGCGWTVIOKRD 200
XX |||||||

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DB 121 RVQSHGLDCTDIKDTIGSVTKTPSGLYTIHPGSSYPEFVCMQMDYRGCGWTVIOKRD 180
XX
XX QY 201 GIIIDFQRLMCDYLDGFGDLLGEFMLGLKKIETVYNQKNTSFMVLVYALSEBDPTLAAASYD 260
XX |||||||
XX DB 181 GIIIDFQRLMCDYLDGFGDLLGEFMLGLKKIETVYNQKNTSFMVLVYALSEBDPTLAAASYD 240
XX
XX QY 261 NFWLEDETREFKMHILGRYSNAGDAFRGLKKEQNANAFSTSDVNDGCRPACLVNGOS 320
XX |||||||
XX DB 241 NFWLEDETREFKMHILGRYSNAGDAFRGLKKEQNANAFSTSDVNDGCRPACLVNGOS 300
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XX QY 321 VKSCSHLHNKTGMWFEBCGLANLNGIHFSGKLLATGIGTWTKNNSPVKIKSVSMKIR 380
XX |||||||
XX DB 301 VKSCSHLHNKTGMWFEBCGLANLNGIHFSGKLLATGIGTWTKNNSPVKIKSVSMKIR 360
XX
XX QY 381 RMYNPFYK 388
XX |||||||
XX DB 361 RMYNPFYK 368
XX
XX RESULT 5
XX AAU14275
XX ID AAU14275 standard; Protein; 326 AA.
XX
XX AC AAU14275;
XX
XX DT 24-OCT-2001 (first entry)
XX
XX XX Human novel protein #146.
XX DE
XX XX Human: novel protein; cytostatic; neuroprotective; vulnerrary; nootropic;
XX KW immunomodulatory; anticancer; osteoporotic; antineoplastic;
XX KW anticonvulsant; antidiabetic; cerebroprotective; antifungal; antiviral;
XX KW antibacterial; antiallergic; dermatological; hemostatic; antiasthmatic;
XX KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
XX KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
XX KW tissue regeneration; immune disorder.
XX
XX XX Homo sapiens.
XX OS
XX XX WO200155437-A2.
XX PN
XX
XX PD 02-AUG-2001.
XX
XX PF 25-JAN-2001; 2001WO-US02623.
XX PR 25-JAN-2000; 2000US-0491404.
XX
XX PA (HYSE-) HYSEQ INC.
XX
XX PI Tang YT, Liu C, Drmanac RT;
XX
XX WPI: 2001-451939/48.
XX DR N-PSDB: AAS22580.
XX
XX PT Isolated polypeptides useful for treating anti-inflammatory diseases,
XX PT nervous system disorders, and for regenerating bone and cartilage -
XX
XX PS Example 4; Page 605; 894pp; English.
XX
XX The invention relates to polynucleotides encoding novel human
XX proteins or their active domains. The polypeptides, polynucleotides and
XX antibodies raised against the polypeptides are used in a method of
XX treatment of a mammal and prevention of disorders caused by the aberrant
XX protein expression or activity. The polypeptides can be used as
XX molecular weight markers, food supplements, and in antibody production.
XX The polypeptides are used to identify compounds which bind to the
XX polypeptides. Polynucleotides of the invention are used as probes and
XX primers, for sequencing, for chromosome or gene mapping, in the
XX production of recombinant proteins, and in generating anti-sense DNA or
XX RNA and in gene therapy. Polypeptides of the invention can be used to
XX target drugs to a tumour, in assays to determine biological activity, to
XX raise antibodies/elicits an immune response, to determine quantitative
XX protein levels, as tissue markers, and to isolate receptors or ligands.

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CC polypeptides of the invention may also be useful in treating platelet
 CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
 CC ligament and/or nerve tissue, wound healing, treating burns, promoting
 CC the proliferation, differentiation and survival of stem cells, as a
 CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
 CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
 CC fungal infection or from autoimmunity, cancer, allergy, asthma,
 CC graft-versus-host disease, eczema, haemophilia, thrombosis,
 CC anti-inflammatory diseases, nervous system disorders, and infection.
 CC The present sequence represents a protein of the invention.

XX
 SO Sequence 326 AA:

Query Match 82.2%; Score 1729; DB 22; Length 326;
 Best Local Similarity 84.0%; Pred. No. 8.4e-167;
 Matches 326; Conservative 0; Mismatches 0; Indels 62; Gaps 1;

QY 1 MMSPSQASLFLVNCIFIGCEVVGQNCVHSTSSVYNIYEDGSNADEKSDNYCKED 60
 DB 1 MMSPSQASLFLVNCIFIGCEVVGQNCVHSTSSVYNIYEDGSNADEKSDNYCKED 60
 QY 61 CEESCDVKTITREKHFMCRLNLSIVSTRSKLLRMMDQOASLDYLSNOVVELM 120
 DB 61 CEESCDVKTITREKHFMCRLNLSIVSTRSKLLRMMDQOASLDYLSNOVVELM 120
 QY 121 NRVLLETFEVRKQDLPFHRPVQSHGLDCTDIKDTIGSVTKPSGLYIIHPGSSYPFE 180
 DB 121 NRVLLETFEVRKQDLPFHRPVQSHGLDCTDIKDTIGSVTKPSGLYIIHPGSSYPFE 180
 QY 181 VMCDMDYRGSGWYIQRIGIIDFORLKCDDYLDGFEDLLGEFMLGLKATFYIYNOKNTS 240
 DB 181 VMCDMDYRGSGWYIQRIGIIDFORLKCDDYLDGFEDLLGEFMLGLKATFYIYNOKNTS 240
 QY 241 FMLYVALESEDDTLAVASYDNFMLEDETRFKMHLGRYSGNAGDAFGLKKEQNONAMPF 300
 DB 221 -----GDAFGLKKEQNONAMPF 238
 QY 301 STSDVDNDGCRPACLVNGQSVKCSHLANKTGWMFNCGLANLNGIHFFSGKLLATGIOW 360
 DB 239 STSDVDNDGCRPACLVNGQSVKCSHLANKTGWMFNCGLANLNGIHFFSGKLLATGIOW 298
 QY 361 GTWTKNNSPVKIKSVSMKIRRMATNPYFK 388
 DB 299 GTWTKNNSPVKIKSVSMKIRRMATNPYFK 326

RESULT 6

AA014511 standard; Protein; 326 AA.

XX AA014511;

XX 24-OCT-2001 (first entry)

XX Human novel protein #382.

XX Human: novel protein; Antianaemic; osteopathic; antiinflammatory;
 KM immunomodulatory; cytosolic; neuroprotective; vulnerrary; nocotropic;
 KM anticonvulsant; antiallergic; ceredroprotective; antifungal; antilivral;
 KM antibacterial; antiallergic; dermatological; haemostatic; antiastrmatic;
 KM chondrolytic; immunogen; antibody; gene therapy; neurological disorder;
 KM Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
 KM tissue regeneration; immune disorder.

XX Homo sapiens.

XX WO200155437-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02623.

PR 25-JAN-2000; 2000US-0491404.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-451939/48.

XX N-PSDB; AAS22816.

PT Isolated polypeptides useful for treating anti-inflammatory diseases,

PS nervous system disorders, and for regenerating bone and cartilage -

XX Example 4; Page 848-849; 894pp; English.

CC The invention relates to polynucleotides encoding novel human
 CC proteins or their active domains. The polypeptides, polynucleotides and
 CC antibodies raised against the polypeptides are used in a method of
 CC treatment of a mammal and prevention of disorders caused by the aberrant
 CC protein expression or activity. The polypeptides can be used as
 CC molecular weight markers, food supplements, and in antibody production.
 CC The polypeptides are used to identify compounds which bind to the
 CC polypeptides. Polynucleotides of the invention are used as probes and
 CC primers, for sequencing, for chromosome or gene mapping, in the
 CC production of recombinant proteins, and in generating anti-sense DNA or
 CC RNA and in gene therapy. Polypeptides of the invention can be used to
 CC target drugs to a tumour, in assays to determine biological activity, to
 CC raise antibodies/elicits an immune response, to determine quantitative
 CC protein levels, as tissue markers, and to isolate receptors or ligands.
 CC Polypeptides of the invention may also be useful in treating platelet
 CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
 CC ligament and/or nerve tissue, wound healing, treating burns, promoting
 CC the proliferation, differentiation and survival of stem cells, as a
 CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
 CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
 CC fungal infection or from autoimmunity, cancer, allergy, asthma,
 CC graft-versus-host disease, eczema, haemophilia, thrombosis,
 CC anti-inflammatory diseases, nervous system disorders, and infection.
 CC The present sequence represents a protein of the invention.

XX
 SO Sequence 326 AA:

Query Match 82.2%; Score 1729; DB 22; Length 326;
 Best Local Similarity 84.0%; Pred. No. 8.4e-167;
 Matches 326; Conservative 0; Mismatches 0; Indels 62; Gaps 1;

QY 1 MMSPSQASLFLVNCIFIGCEVVGQNCVHSTSSVYNIYEDGSNADEKSDNYCKED 60
 DB 1 MMSPSQASLFLVNCIFIGCEVVGQNCVHSTSSVYNIYEDGSNADEKSDNYCKED 60
 QY 61 CEESCDVKTITREKHFMCRLNLSIVSTRSKLLRMMDQOASLDYLSNOVVELM 120
 DB 61 CEESCDVKTITREKHFMCRLNLSIVSTRSKLLRMMDQOASLDYLSNOVVELM 120
 QY 121 NRVLLETFEVRKQDLPFHRPVQSHGLDCTDIKDTIGSVTKPSGLYIIHPGSSYPFE 180
 DB 121 NRVLLETFEVRKQDLPFHRPVQSHGLDCTDIKDTIGSVTKPSGLYIIHPGSSYPFE 180
 QY 181 VMCDMDYRGSGWYIQRIGIIDFORLKCDDYLDGFEDLLGEFMLGLKATFYIYNOKNTS 240
 DB 181 VMCDMDYRGSGWYIQRIGIIDFORLKCDDYLDGFEDLLGEFMLGLKATFYIYNOKNTS 220
 QY 241 FMLYVALESEDDTLAVASYDNFMLEDETRFKMHLGRYSGNAGDAFGLKKEQNONAMPF 300
 DB 221 -----GDAFGLKKEQNONAMPF 238
 QY 301 STSDVDNDGCRPACLVNGQSVKCSHLANKTGWMFNCGLANLNGIHFFSGKLLATGIOW 360
 DB 239 STSDVDNDGCRPACLVNGQSVKCSHLANKTGWMFNCGLANLNGIHFFSGKLLATGIOW 298
 QY 361 GTWTKNNSPVKIKSVSMKIRRMATNPYFK 388
 DB 299 GTWTKNNSPVKIKSVSMKIRRMATNPYFK 326

PR 06-SEP-2000; 2000US-230514P.
 PR 06-SEP-2000; 2000US-230515P.
 PR 06-SEP-2000; 2000US-230517P.
 PR 06-SEP-2000; 2000US-230518P.
 PR 06-SEP-2000; 2000US-230519P.
 PR 06-SEP-2000; 2000US-230595P.
 PR 06-SEP-2000; 2000US-230597P.
 PR 06-SEP-2000; 2000US-230598P.
 PR 06-SEP-2000; 2000US-230599P.
 PR 06-SEP-2000; 2000US-230610P.
 PR 06-SEP-2000; 2000US-230865P.
 PR 06-SEP-2000; 2000US-230988P.
 PR 06-SEP-2000; 2000US-230989P.
 PR 07-SEP-2000; 2000US-230951P.
 PR 07-SEP-2000; 2000US-231163P.
 PR 07-SEP-2000; 2000US-231167P.
 XX (INCYTE GENOMICS INC.)
 PA Jackson S, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL,
 PI Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR,
 PI Momiyama MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM,
 PI Gerstin EH, Peralta CH, David MH, Panzer SR, Flores V, Dafio A,
 PI Marwaha R, Chen AJ, Chang SC, Au AP, Imman RR.
 XX WPI: 2002-527544/56.
 DR N-PSDB; AB072639.
 XX
 PT Novel human disease detection and treatment polypeptide, useful in
 PT diagnosis, prevention or treatment of cell proliferative disorders e.g.
 PT arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder
 PT e.g. AIDS
 PS
 PS Claim 14; Page 576-577; 618pp: English.
 XX
 CC The invention relates to an isolated human disease detection and
 CC treatment (MDT) polypeptide (I) selected from a polypeptide having a
 CC sequence selected from 254 sequences (ABP51231-ABP51484) given in the
 CC specification, a naturally occurring polypeptide comprising a sequence
 CC having at least 90% identity to (I) or a biologically active or
 CC immunogenic fragment of (I). (I) is useful for screening a compound for
 CC effectiveness as an agonist or antagonist, for screening a compound that
 CC specifically binds (I) or modulates the activity of (I), and for
 CC preparing a polyclonal or monoclonal antibody by hybridoma technology.
 CC Nucleic acids (II) (AB072449-AB072700) encoding (I) are useful for
 CC screening a compound for effectiveness in altering expression of a target
 CC polynucleotide comprising oligonucleotides and antibodies are useful for
 CC detecting MDT in a sample or for assessing toxicity of a test compound,
 CC in a diagnostic test for a condition or a disease associated with the
 CC expression of MDT in a biological sample, for detecting (I) in a sample,
 CC and for purifying (I) from a sample. A composition comprising (I), an
 CC agonist or antagonist is useful for treating a disease or condition
 CC associated with decreased or increased expression of functional MDT.
 CC (I) or (II) are useful for diagnosing, treating or preventing disorders
 CC associated with aberrant expression of MDT, where the disorders are
 CC selected from a cell proliferative disorder such as arteriosclerosis,
 CC cirrhosis, hepatitis, psoriasis, and cancer and an
 CC autoimmune/inflammatory disorder such as AIDS, Addison's disease,
 CC allergy, anaemia, asthma, atherosclerosis, gout, multiple sclerosis or
 CC rheumatoid arthritis. (II) are useful for creating knockin humanised or
 CC animals or transgenic animals to model human diseases, in somatic or
 CC germ-line gene therapy, to generate a transcript image of a tissue or cell
 CC type, for detecting differences in the chromosomal location due to
 CC translocation or inversion among normal, carrier or affected individuals
 CC and as hybridisation probes for mapping naturally occurring genomic
 CC sequences.
 XX
 SQ Sequence 335 AA;
 Query Match 81.3%; Score 1711.5; DB 23; Length 335;
 Best Local Similarity 83.0%; Pred. No. 5.3e-165;
 Matches 322; Conservative 0; Mismatches 1; Indels 65; Gaps 1;

QY 1 MMSPSQASLFLNLCIFCGEVQGCYVHSTDSVYNIIVEDGSNAKDESKNDPVCKED 60
 Db 13 MMSPSQASLFLNLCIFCGEVQGCYVHSTDSVYNIIVEDGSNAKDESKNDPVCKED 72
 QY 61 CEESCDVTKITREKHEKHCNKLNSIVSYRSTKILRNMMDDQASLDVLSNOVELM 120
 Db 73 CEESCDVTKITREKHEKHCNKLNSIVSYRSTKILRNMMDDQASLDVLSNOVELM 127
 QY 121 NRVLLLTTEVERKQIDPEPHRPVOSHGDCTDIDITIGSVTKTSPGLEYIIHPESSYPFE 180
 Db 128 ----- 127
 QY 181 VMCDMDYRGCGWYIYQKRIDGIIIDFQRIWCDYLDGFGDLGCEFWLGKRIYVQNKNTS 240
 Db 128 VMCDMDYRGCGWYIYQKRIDGIIIDFQRIWCDYLDGFGDLGCEFWLGKRIYVQNKNTS 187
 QY 241 FMLYVALESEDDTLAYASYDNFWEDEDFRFRKMLGRYSNAGAFRGLEKEDNONMPE 300
 Db 188 FMLYVALESEDDTLAYASYDNFWEDEDFRFRKMLGRYSNAGAFRGLEKEDNONMPE 247
 QY 301 STSDVDNDGCRPACLVNGSVKSCSHLHNTGMMFNECGLANLINGIHHSGLATGIGW 360
 Db 248 STSDVDNDGCRPACLVNGSVKSCSHLHNTGMMFNECGLANLINGIHHSGLATGIGW 307
 QY 361 GTWTRKNSPVKIKSVSMKIRRMVNPYFK 388
 Db 308 GTWTRKNSPVKIKSVSMKIRRMVNPYFK 335

RESULT 9
 AAB82593
 ID AAB82593 standard; Protein; 306 AA.
 XX
 AC AAB82593;
 XX
 DT 02-OCT-2001 (first entry)
 XX

Human prothrombinase-like polypeptide splice variant mature protein.
 KW Prothrombinase-like polypeptide: human; haemostatic; cardiac;
 KW nephrotropic; antidiabetic; hepatotropic; antiviral; cytosolic;
 KW antidiabetic; antileukemic; antileukemic; osteoporosis;
 KW immunomodulatory; antineutrophic; antineutrophic; antineutrophic;
 KW thrombolytic; diagnosis; therapy.
 XX
 OS Homo sapiens.
 XX
 FN W0200153456-A2.
 XX
 PD 26-JUL-2001.
 XX

22-DEC-2000; 2000WO-US35061.
 XX
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-JAN-2000; 2000US-0491404.
 PR 25-APR-2000; 2000US-052317.
 PR 17-JUN-2000; 2000US-0596196.
 PR 31-AUG-2000; 2000US-0643313.
 XX

(HYSE-) HYSE INC.
 PA Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
 PI Arterburn MC, Tang YR, Liu C, Drmanac R;
 PI
 XX WPI: 2001-483140/52.
 DR N-PSDB; AAB826237.
 XX

Novel prothrombinase-like polypeptides and polynucleotides useful in
 PT diagnosing and treating e.g. myocardial infarction and diabetes -
 PS Claim 10; Page 135-136; 140pp: English.
 XX

The present sequence is that of the mature portion of a novel

RESULT 11
 AAB82392
 ID AAB82592 standard; Protein; 240 AA.
 XX
 AC AAB82592;
 XX
 DT 02-OCT-2001 (first entry)
 XX
 DE Human prothrombinase-like polypeptide splice variant domain.
 XX
 KM Prothrombinase-like polypeptide; human; haemostatic; cardiant;
 KM nephrotropic; antidiabetic; hepatotropic; antiviral; cytosolic;
 KM antitartaric; antitumor; antitumor; osteoporosis;
 KM immunomodulatory; antirheumatic; antitartaric; antinflammatory;
 KM thrombolytic; diagnosis; therapy; blood coagulation.
 XX
 OS Homo sapiens.
 XX
 PN WO200153456-A2.
 XX
 PD 26-JUL-2001.
 XX
 PF 22-DEC-2000; 2000MO-US35061.
 XX
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-JAN-2000; 2000US-0491404.
 PR 25-APR-2000; 2000US-0552317.
 PR 17-JUN-2000; 2000US-0596196.
 PR 31-AUG-2000; 2000US-0643313.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Haley DA, Boyle BU, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
 PI Atterburn MC, Tang YF, Liu C, Drmanac R;
 XX
 DR WPI: 2001-483140/52.
 DR N-PSDB; AAB26237.
 XX
 PT Novel prothrombinase-like polypeptides and polynucleotides useful in
 PT diagnosing and treating e.g. myocardial infarction and diabetes -
 XX
 PS Claim 10; Page 134-135; 140pp; English.
 XX
 CC The present sequence is that of the blood coagulation domain of a
 CC secreted, soluble splice variant (see AAB82590) of novel human
 CC prothrombinase-like polypeptide (PLP). PLP polynucleotides and
 CC polypeptides, including those comprising the present domain of the
 CC PLP splice variant, can be used in the diagnosis, treatment and/or
 CC prevention of diseases associated with the dysregulation of
 CC coagulation pathways, such as haemophilia, myocardial infarction,
 CC glomerular disease, diabetes, fulminant viral hepatitis and
 CC atherosclerosis. They may also be beneficial in the treatment of
 CC viral infections and some forms of cancer. A claimed method of
 CC treating a subject in need of enhanced PLP activity or expression
 CC involves the administration of PLP, a PLP agonist or a
 CC polynucleotide encoding PLP. A claimed method of treating a subject
 CC having need to inhibit activity or expression of PLP involves the
 CC administration of a PLP antagonist, a polynucleotide that inhibits
 CC expression of a PLP polynucleotide, or a polypeptide that competes
 CC with the PLP for its ligand. The polypeptides can also be used to
 CC raise antibodies, as food supplements, and to screen for agonists
 CC and antagonists.
 XX
 SQ Sequence 240 AA;
 XX
 Query Match 60.1%; Score 1265; DB 22; Length 240;
 Best Local Similarity 79.3%; Pred. No. 7,4e-120;
 Matches 240; Conservative 0; Mismatches 0; Indels 62; Gaps 1;
 QY 82 NLAQSIYSTRSTKRLRNMMDEQASLDYLSNOVNLNMRVLLTTEVFRKQDPPFHR 141
 DB 1 NLAQSIYSTRSTKRLRNMMDEQASLDYLSNOVNLNMRVLLTTEVFRKQDPPFHR 60

QY 142 PVQSHGLDCTDIDKTIGSVTKTPSGLYIHPDESSYPEPVNCDMDYRGCGMTVIQKRIDG 201
 DB 61 PVQSHGLDCTDIDKTIGSVTKTPSGLYIHPDESSYPEPVNCDMDYRGCGMTVIQKRIDG 120
 QY 202 IIDFORLWCDYLDGFGDLGFEWGLKRIYIVQNKTSFPLLYALSEDDTLAYASDN 261
 DB 121 IIDFORLWCDYLDGFGDLGFEWGLKRIYIVQNKTSFPLLYALSEDDTLAYASDN 139
 QY 262 FWLEDETRFEFMHLGRYSNAGDAFRLGLKEDNPNAMPFSTSDVDNDGCRPACLVNQSIV 321
 DB 140 -----GDAPFRGLKEDNPNAMPFSTSDVDNDGCRPACLVNQSIV 178
 QY 322 KCSCHLNKGTGWMEFNEGLANLNGIHPFSGKLTATGIQWGTWTKNNSPVKIKSVSMKIRR 381
 DB 179 KCSCHLNKGTGWMEFNEGLANLNGIHPFSGKLTATGIQWGTWTKNNSPVKIKSVSMKIRR 238
 QY 382 MY 383
 DB 239 MY 240
 RESULT 12
 AABG22365
 ID AABG22365 standard; Protein; 141 AA.
 XX
 AC AABG22365;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #22365.
 XX
 KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001MO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YF;
 PI Drmanac RT, Liu C, Tang YF;
 XX
 DR WPI: 2001-639362/73.
 DR N-PSDB; AAS86552.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID NO 52724; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 141 AA:
Query Match 30.1%; Score 634; DB 22; Length 141;
Best Local Similarity 64.3%; Pred. No. 4.3e-56;
Matches 119; Conservative 1; Mismatches 3; Indels 62; Gaps 1;
QY 178 PEVWCDMDYRGSGWTVYOKRIDGIIDFQRLMCDYLDGSGDLGERWLGKRIFFYVNOK 237
DB 9 PEVWCDMDYRGSGWTVYOKRIDGIIDFQRLMCDYLDGSGDL----- 51
QY 238 NTFMVLVALESEDDTLAAYSDNFWLEDETRFFKMHGLGRYSGNAGDAPRGLKKEDNNA 297
DB 52 -----GDAFLFLKKEDNNA 66
QY 238 MPEFSDVDNDGCRPACLYNGSVKSCSHLHNTGWFNECGLANLNGIHFSGKLLATG 357
DB 67 MPEFSDVDNDGCRPACLYNGSVKSCSHLHNTGWFNECGLANLNGIHFSGKLLATG 126
QY 358 IQWGT 362
DB 127 IQWGT 131
RESULT 13
ABG22361
ID ABG22361 standard; Protein: 138 AA.
XX
AC ABG22361;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #22352.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PE 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS86548.
XX
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID NO 52720; 103pp; English.
CC
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The

CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 138 AA:
Query Match 29.9%; Score 628.5; DB 22; Length 138;
Best Local Similarity 64.6%; Pred. No. 1.5e-55;
Matches 126; Conservative 1; Mismatches 3; Indels 65; Gaps 1;
QY 1 MMSPGASLFLNVCIFTCGEVYVGGNCVHNSDSSVNVIVEDGSNAKDESKNDYCKED 60
DB 9 MMSPSLALLFLFNVCIFTCGEVYVGGNCVHNSDSSVNVIVEDGSNAKDESKNDYCKED 68
QY 61 CEESCDVKTITREKHEKFCRLNLSIVYSTRTKLLRNMDDEOASLDYSNOVNELM 120
DB 69 CEESCDVKTITREKHEKFCRLNLSIVYSTRTKLLRNMDDEOASLDYSNO----- 123
QY 121 NRVLLITTEVFRKQDPEFHPVQSHGLDCTDIKDTIGSVTKPSGLYIIHPEGSSYPE 180
DB 124 ----- 123
QY 181 VMCDMDYRGSGWTVI 195
DB 124 VMCDMDYRGSGWTVI 138
RESULT 14
ABG22364
ID ABG22364 standard; Protein: 116 AA.
XX
AC ABG22364;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #22355.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PE 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS86551.
XX
XX
PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 PS Claim 20; SEQ ID NO 52723; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expressions or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 116 AA;
 Query Match 24.8%; Score 521; DB 22; Length 116;
 Best Local Similarity 93.1%; Pred. No. 9.6e-45;
 Matches 95; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 161 TKRTSGLYIIHPESSYFPEVCMQDRGGGWYIQRKIDIIIPQRLMCIYLDGFDLL 220
 DB 13 TKRTSGLYIIHPESSYFPEVCMQDRGGGWYIQRKIDIIIPQRLMSDYLDGFDLV 72
 QY 221 GEFMLGLKRIYIVNOKNTSFLVVALESEDDTLAVASYDNF 262
 DB 73 GEFMLGLKRIYIVNOKNTSFLVVALESEDDTLAVASYDNF 114
 RESULT 15
 AAY26196
 ID AAY26196 standard; Protein: 491 AA.
 XX
 AC AAY26196;
 XX
 DT 03-NOV-1999 (first entry)
 XX
 DE Human zapo3 protein.
 XX
 KW Human zapo3 protein; angiotensin-1, angiotensin-2; covalently linked;
 KW moiety; affinity tag; toxin; radionuclide; enzyme; fluorophore; multimer;
 KW coiled coil domain; carboxyl-terminal fibrinogen-like domain; angiogenic;
 KW haematopoietic; mitogenic activity; angiogenic; inhibitor;
 KW endocrine-vascular cell association; revascularisation; DNA probe;
 KW neuronal degeneration; anti-zapo3 antibody.
 XX
 OS Homo sapiens.
 XX
 FH Key location/Qualifiers
 FT Peptide 1..21
 FT /label= Secretory_Signal_Sequence
 FT Peptide 43..48
 FT /label= Immunogen
 FT /note= "For production of antibodies"
 FT Peptide 93..98
 FT /label= Immunogen
 FT /note= "For production of antibodies"
 FT Peptide 120..125
 FT /label= Immunogen

FT Peptide /note= "For production of antibodies"
 FT 421..426
 FT /label= Immunogen
 FT /note= "For production of antibodies"
 FT Peptide 422..427
 FT /label= Immunogen
 FT /note= "For production of antibodies"
 FT Domain 279..490
 FT /label= "Fibrinogen-like domain
 FT /note= "Homologous to residues 631-864 of human
 FT fibrinogen alpha chain"
 FT Domain 63..253
 FT /label= Amino-terminal-coiled-coil-domain
 FT MISC-difference 280
 FT /note= "Conserved cysteine residue"
 FT MISC-difference 309
 FT /note= "Conserved cysteine residue"
 FT MISC-difference 432
 FT /note= "Conserved cysteine residue"
 FT MISC-difference 445
 FT /note= "Conserved cysteine residue"
 XX
 PN W09940193-A1.
 XX
 PD 12-AUG-1999.
 XX
 PF 03-FEB-1999; 99WO-US02303.
 XX
 PR 04-FEB-1998; 98US-0018258.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Holloway JL, Shoemaker KE;
 XX WPI: 1999-508503/42.
 DR N-PSDB: AAX80866.
 XX
 PT Human angiotensin homologue, ZAPO3 useful for study and regulation
 of angiogenesis
 XX
 PS Claim 1; Page 65-67; 78pp; English.
 XX
 CC The present sequence is a human zapo3 protein. Zapo3 protein exhibits
 CC significant amino acid sequence homology to angiotensin-1 and 2. It is
 CC covalently linked to a moiety chosen from affinity tags, toxins,
 CC radionuclides, enzymes and fluorophores. The protein is assembled as a
 CC multimer and is characterized by an amino-terminal coiled coil domain and
 CC a carboxyl-terminal fibrinogen-like domain. Zapo3 has angiogenic,
 CC haematopoietic and mitogenic activity. It is useful in the study and
 CC regulation of angiogenesis, and for developing inhibitors of
 CC angiogenesis. It is possibly involved in modulation of endocrine-vascular
 CC cell association and may be used therapeutically to stimulate the
 CC revascularisation of tissue, to promote angiogenesis and prevent neuronal
 CC degeneration. DNA probes and anti-zapo3 antibodies can be used to detect
 CC sites of angiogenesis.
 XX
 SQ Sequence 491 AA;
 Query Match 20.2%; Score 425; DB 20; Length 491;
 Best Local Similarity 26.9%; Pred. No. 4.9e-34;
 Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;
 QY 44 SNADDESKNDVCKEDCEESCDYKTKITRE-EKHFMGRNIONSTVSTRSTKILRRMM 102
 DB 68 TKGDASTIKMTIRMDLENIKDVLSROKREIDVQLVVDGNTVNEVKILKRRESRMN 127
 QY 103 DE-QQASIDYL-----SNQVWELMNRVLLTTE----- 129
 DB 128 SRVQLVWQGLHEIRKRDNLSLELSQLENKTLNVTTELKMATRYRELEVAYASITDLYN 187
 QY 130 -----VFRKQ---LDP-----FPHRPVQSHGL----- 148
 DB 188 NQSVITLLEECLEIFSRDPTHVSPLVQVVPQHIPSQGYTFGLLGNEIQDPGYPR 247

QY 149 DCTDIDKTIIGSVTKRP-----SGLYIHPGSSYTFEY 181
| | | | |
Db 248 DLMPPDLATSPTKSPFKIPVYTFINEGPPKDCQAKKEAGHSVSGIYMIKPENSGPMOL 307
| | | | |
QY 182 MCDMDYRGSGWTVIOKRIDGIIDFORLMCDYLDGFDLGEFWLGLKIFYYIVNOKNTSF 241
| | | | |
Db 308 WCENSLDPGSGWTVIOKRIDGVSVEFFRNMENTYKKGFGNIDGEYWLGLENTYMLSNQDN--Y 365
| | | | |
QY 242 MLYVALESEDDTLAYASYDNFMLEDETRFEFKMHLGRYSGNAGDAFRGLKEDNQAMPFS 301
| | | | |
Db 366 KLIIELEDMSDKRYVAEYSSFLPESEFEYRLGLTYOGNAGDSMMW-----HNGKQFT 419
| | | | |
QY 302 TSDVDNDGCRPACLVNGQSVKSCSHLHNKTGMWFNECGLANLNGIHFSGLLA---TGI 358
| | | | |
Db 420 TIDRDKD-----MTAGNCAHFH-KGWMYFNACAHNSNLNGVWYRGGHYRSKHODGI 468
| | | | |
QY 359 QMGWTWKNSPYKIKSVSMKIR 380
| | | | |
Db 469 FWAIEY--RGSYSLSRAVQMMIK 488
| | | | |

Search completed: December 16, 2002, 17:34:15
Job time : 35.873 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 16, 2002, 17:27:03 ; Search time 32.127 Seconds
(without alignments)
1526.325 Million cell updates/sec

Title: US-09-596-196-9

Perfect score: 2000
Sequence: 1 EVVQNCVHSTSSVNVIV.....PVKIKSVSMKIRMYNPFYK 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq.101002.*
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20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2000	100.0	368	22	AA882589 Human prothrombina
2	2000	100.0	368	22	AA882584 Human prothrombina
3	1996	99.8	388	22	AA772622 Human angiotensin
4	1982	99.1	388	23	AA877546 Human polypeptide
5	1625	81.2	306	22	AA882593 Human prothrombina
6	1625	81.2	326	22	AAU14275 Human novel protei
7	1625	81.2	326	22	AAU14511 Human prothrombina
8	1625	81.2	326	22	AA882590 Human prothrombina
9	1607.5	80.4	335	22	ABP51422 Human MDR1 SER ID
10	1299	65.0	237	22	AA882582 Human prothrombina

11	1265	63.2	240	22	AA882592 Human prothrombina
12	634	31.7	141	22	ABG22365 Novel human diagno
13	538.5	26.9	138	22	ABG22361 Novel human diagno
14	521	26.1	116	22	ABG22364 Novel human diagno
15	425	21.2	491	20	AA726196 Human zapo3 protei
16	425	21.2	491	20	AA705397 Human TIE-2 ligand N
17	425	21.2	491	21	AA847996 Angiotensin-like
18	425	21.2	491	21	AA824393 Human PRO188 prote
19	425	21.2	491	21	AA69483 Amino acid sequenc
20	425	21.2	491	21	AA68761 An angiotensin-re
21	425	21.2	491	22	AAU12310 Human PRO188 polyp
22	425	21.2	491	22	AA60340 Human neovasculari
23	425	21.2	491	22	AA853067 Human angiogenesis
24	425	21.2	491	23	AAE19826 Human TIE-2 ligand N
25	421	21.1	491	21	AA44841 Human secreted pro
26	420	21.0	491	21	AA848000 Protein encoded by
27	414	20.7	245	22	AA899915 Human polypeptide
28	413.5	20.7	439	20	AA882335 Human prothrombina
29	405.5	20.3	432	20	AA882336 Mouse prothrombina
30	403.5	20.2	497	17	AAW01410 Human TIE-2 ligand
31	403.5	20.2	497	17	AA894604 Human TIE-2 ligand
32	401.5	20.1	380	21	AA90401 Amino acid sequenc
33	400.5	20.0	493	21	AA841712 Mouse angiotensin
34	400.5	20.0	386	20	AA59881 Human ORF1476
35	400	20.0	493	20	AA505396 Human normal uteru
36	400	20.0	493	21	AA847997 Human TIE-2 ligand N
37	400	20.0	493	21	AA847997 Human TIE-2 ligand N
38	400	20.0	493	21	AA70745 PSE-3 protein enc
39	400	20.0	493	21	AA545999 Human scarface 1 p
40	400	20.0	493	22	AAU12305 Human PRO196 polyp
41	400	20.0	493	22	AA831179 Amino acid sequenc
42	400	20.0	493	22	AA851329 Human 410 angioten
43	400	20.0	493	23	AA866340 Human angiotensin
44	400	20.0	493	23	AAU14786 Human matrix-remod
45	400	20.0	493	23	AAE19825 Human TIE-2 ligand N

ALIGNMENTS

RESULT 1	AA882589	standard; Protein; 368 AA.
ID	AA882589	
XX	AA882589;	
AC	02-OCT-2001	(first entry)
XX		
DE	Human prothrombinase-like polypeptide (mature protein).	
XX		
DE	Prothrombinase-like polypeptide: human; haemostatic; cardiant;	
KW	nephrotropic; antidiabetic; hepatotropic; antiviral; cytostatic;	
KW	antitesterioscleotic; antitumor; vulnary; osteoporosis;	
KW	immunomodulatory; antirheumatic; antithrombotic; antiinflammatory;	
KW	thrombolytic; diagnosis; therapy.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Domain	161..197
FT	Domain	/note="fibrinogen beta/gamma chain"
FT	Domain	202..214
FT	Domain	/note="fibrinogen beta/gamma chain"
FT	Domain	251..265
FT	Domain	/note="fibrinogen beta/gamma chain"
FT	Domain	304..333
FT	Domain	/note="fibrinogen beta/gamma chain"
PN	WO200153456-A2.	
XX		
PD	26-JUL-2001.	
XX		
PF	22-DEC-2000; 2000WO-US35061.	

CC haemophilia, myocardial infarction, glomerular disease, diabetes,
 CC fulminant viral hepatitis and atherosclerosis. They may also be
 CC beneficial in the treatment of viral infections and some forms of
 CC cancer. A claimed method of treating a subject in need of enhanced
 CC PLP activity or expression involves the administration of PLP, a
 CC PLP agonist or a polynucleotide encoding PLP. A claimed method of
 CC treating a subject having need to inhibit activity or expression of
 CC PLP involves the administration of a PLP antagonist, a
 CC polynucleotide that inhibits expression of a PLP polynucleotide,
 CC or a polypeptide that competes with the PLP for its ligand. The
 CC polypeptides can also be used to raise antibodies, as food
 CC supplements, and to screen for agonists and antagonists.

XX Sequence 388 AA;

Query Match 100.0%; Score 2000; DB 22; Length 388;
 Best Local Similarity 100.0%; Pred. No. 2e-195;
 Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVVQNCVHSTDSVVNIYEDGSAKDESKNDYCKEDCESCDVTKITREKHFMC 60
 DB 21 EVVQNCVHSTDSVVNIYEDGSAKDESKNDYCKEDCESCDVTKITREKHFMC 80
 QY 61 RNLQNSIVSTRSTKLLRNMMDEQASLDYLSNOVNEIMNRVLLTTEVFRKQIDPPH 120
 DB 81 RNLQNSIVSTRSTKLLRNMMDEQASLDYLSNOVNEIMNRVLLTTEVFRKQIDPPH 140
 QY 121 RPYVSHGIDCDIKDTIGSVTKTPSGLYIHPGSSYPFEVCMCDYRGGGTGYOKRID 180
 DB 141 RPYVSHGIDCDIKDTIGSVTKTPSGLYIHPGSSYPFEVCMCDYRGGGTGYOKRID 200
 QY 181 GIIDFQRLMCDYLDGFDLGEFNLGKIFYYVQKNTSFMLYVALESEDDTLAVASYD 240
 DB 201 GIIDFQRLMCDYLDGFDLGEFNLGKIFYYVQKNTSFMLYVALESEDDTLAVASYD 260
 QY 241 NFWLEDETRFFKMLGKRYSGNAGAFRLKKEQNONAMPESTSDVNDGCRPACLVNQS 300
 DB 261 NFWLEDETRFFKMLGKRYSGNAGAFRLKKEQNONAMPESTSDVNDGCRPACLVNQS 320
 QY 301 VKSCSHLHNTKGMWFNECGLANLNGIHFSGLKATGIGMTWTKNNSPVIRKYSMKIR 360
 DB 321 VKSCSHLHNTKGMWFNECGLANLNGIHFSGLKATGIGMTWTKNNSPVIRKYSMKIR 380
 QY 361 RMYNPFYK 368
 DB 381 RMYNPFYK 388

RESULT 3
 AAY72622
 ID AAY72622 standard; Protein; 388 AA.

XX AAY72622;

XX 02-MAY-2001 (first entry)

DE Human angiotensin protein, CG144.

XX Human: angiotensin; angiotensin; gene therapy; CG144;
 KW vascular stability; neovascularisation; nutritional supplement; therapy;
 KW myocardial infarction; proliferative retinopathy; atherosclerosis;
 KW coronary heart disease; arterial ischaemia; bone disorder; cancer;
 KW abnormal vascular growth; anaemia; chronic inflammation; immune disorder;
 KW haematopoiesis related disorder; coagulation disorder; leukaemia;
 KW cytoskeletal; vasotropic; food supplement; nervous system disorder;
 KW drug screening.

XX Homo sapiens.

XX Key location/Qualifiers

FT Peptide 1..22
 FT /label- Signal_peptide
 FT Protein 23..388

FT Domain /note- "Mature angiotensin protein, CG144"
 FT 193..230
 FT /note- "Fibrinogen domain"
 FT 234..247
 FT /note- "Fibrinogen domain"
 FT 283..301
 FT /note- "Fibrinogen domain"
 FT 307..321
 FT /note- "Fibrinogen domain"
 FT 337..366
 FT /note- "Fibrinogen domain"

XX WO200105825-A2.

XX 25-JAN-2001.

XX 17-JUL-2000; 2000WO-US19429.

XX 16-JUL-1999; 99US-0354881.

XX (HYSE-) HYSEQ INC.

XX Ballinger DG, Montgomery JR;

XX WPI: 2001-091966/10.

XX N-PSDB: AAD02607.

XX Human angiotensin protein and DNA encoding sequences useful for
 FT preventing, treating or ameliorating a medical condition in a mammalian
 FT subject e.g. arthritis and cancer -

XX Claim 10; Page 111-112; 132pp; English.

XX The present sequence is human angiotensin protein, CG144.
 CC The present invention relates to human angiotensin polypeptides such
 CC as CG006, CG007, CG015, CG144 and CG250. The angiotensin polynucleotides
 CC are used as hybridisation probes, for chromosome and gene mapping, to
 CC identify polymorphism and for recombinant protein production.
 CC Angiotensin may be useful for modulating vascular stability and
 CC neovascularisation associated with various pathologies. It is used as a
 CC nutritional supplement, molecular weight marker and in gene therapy. It
 CC is also used for preventing, treating or ameliorating angiotensin
 CC related disorders such as myocardial infarction, proliferative
 CC retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia,
 CC bone disorders (e.g., osteoporosis), abnormal vascular growth, cancer,
 CC anaemia and chronic inflammation (e.g., asthma and arthritis) and immune
 CC disorders (e.g., inflammatory reactions and autoimmune diseases),
 CC haematopoiesis related disorders (e.g., myeloid or lymphoid cell
 CC deficiencies), coagulation disorders, leukaemias and nervous system
 CC disorders. It is also used in drug screening techniques for screening
 CC compounds which are able to modulate the expression or activity of
 CC angiotensin. The compounds can also be used to treat diseases and
 CC disorders.

XX Sequence 388 AA;

Query Match 99.8%; Score 1996; DB 22; Length 388;
 Best Local Similarity 99.7%; Pred. No. 5.2e-195;

Matches 367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVVQNCVHSTDSVVNIYEDGSAKDESKNDYCKEDCESCDVTKITREKHFMC 60
 DB 21 EVVQNCVHSTDSVVNIYEDGSAKDESKNDYCKEDCESCDVTKITREKHFMC 80
 QY 61 RNLQNSIVSTRSTKLLRNMMDEQASLDYLSNOVNEIMNRVLLTTEVFRKQIDPPH 120
 DB 81 RNLQNSIVSTRSTKLLRNMMDEQASLDYLSNOVNEIMNRVLLTTEVFRKQIDPPH 140
 QY 121 RPYVSHGIDCDIKDTIGSVTKTPSGLYIHPGSSYPFEVCMCDYRGGGTGYOKRID 180
 DB 141 RPYVSHGIDCDIKDTIGSVTKTPSGLYIHPGSSYPFEVCMCDYRGGGTGYOKRID 200
 QY 181 GIIDFQRLMCDYLDGFDLGEFNLGKIFYYVQKNTSFMLYVALESEDDTLAVASYD 240

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Db 201 GIIDFQRLMCDYLDGFGDILLGEFWMGLKKIFLYVNOKNTSFMLYVALESEDDTLAAYSD 260
Qy 241 NFWLEDETRFEFKMLHGRYSGNAGDAFRGLKKEEDNONAMPSTSDVNDGCRPACLVNGOS 300
Db 261 NFWLEDETRFEFKMLHGRYSGNAGDAFRGLKKEEDNONAMPSTSDVNDGCRPACLVNGOS 320
Qy 301 VKSCSHLNKKTGMWFMNCGLANLNGIHHSFSGKLATGIGMGTWTKNNSPVKIKSVSMKIR 360
Db 321 VKSCSHLNKKTGMWFMNCGLANLNGIHHSFSGKLATGIGMGTWTKNNSPVKIKSVSMKIR 380
Qy 361 RMYNPFYK 368
Db 381 RMYNPFYK 388

RESULT 4
AB877546
ID ABB77546 standard; Protein; 388 AA.
XX
AC ABB77546;
XX
DT 05-AUG-2002 (first entry)
XX
DE Human polypeptide SEQ ID NO 2.
XX
KW Human; collagen II; aggrecan; antiarthritic; cartilage;
KM arthritis deformans.
XX
OS Homo sapiens.
XX
PN WO200242448-A1.
XX
PD 30-MAY-2002.
XX
PF 21-NOV-2001; 2001WO-JP10150.
XX
PR 22-NOV-2000; 2000JP-0356378.
XX
PA (YAMA ) YAMANOUCHI PHARM CO LTD.
XX
PI Yaenunaga K;
XX
PI WPI: 2002-463631/49.
DR N-PSDB; ABL60374.
XX
PT Human polypeptide promoting collagen II and aggrecan production for
PS treatment and prevention of arthritis deformans.
XX
PS Claim 1; Page 56-57; 72pp; Japanese.
XX
CC The invention relates to human polypeptide (ABB77546) promoting collagen
CC II and/or aggrecan activity created by addition, deletion and/or
CC substitution. The polypeptide has antiarthritic activity and promotes
CC collagen II and aggrecan production in cartilage cells. It is useful for
CC treatment and prevention of arthritis deformans.
XX
SQ Sequence 388 AA:
Query Match 99.1%; Score 1982; DB 23; Length 388;
Best Local Similarity 99.5%; Pred. No. 1,4e-193;
Matches 366; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EYVQNCVNHSTSDSVYVIVEDGSSNAKDKSNDYCKKDCEDSCDYKTKITREEHFMK 60
Db 21 EAVQNCVNHSTSDSVYVIVEDGSSNAKDKSNDYCKKDCEDSCDYKTKITREEHFMK 80
Qy 61 RMLQNSIYVSTSTKRLKLNMDDEOASLDYLSNOVNEIMNRYLLTTEVFRKQLDPFH 120
Db 81 RMLQNSIYVSTSTKRLKLNMDDEOASLDYLSNOVNEIMNRYLLTTEVFRKQLDPFH 140
Qy 121 RPVQSHGLDCTDIDKIDTIGSVTKPSGLYIIHFGSSYPFEVACMDMYRGSGWTVIQRI 180
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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Db 141 RPVQSHGLDCTDIDKIDTIGSVTKPSGLYIIHFGSSYPFEVACMDMYRGSGWTVIQRI 200
Qy 181 GIIDFQRLMCDYLDGFGDILLGEFWMGLKKIFLYVNOKNTSFMLYVALESEDDTLAAYSD 240
Db 201 GIIDFQRLMCDYLDGFGDILLGEFWMGLKKIFLYVNOKNTSFMLYVALESEDDTLAAYSD 260
Qy 241 NFWLEDETRFEFKMLHGRYSGNAGDAFRGLKKEEDNONAMPSTSDVNDGCRPACLVNGOS 300
Db 261 NFWLEDETRFEFKMLHGRYSGNAGDAFRGLKKEEDNONAMPSTSDVNDGCRPACLVNGOS 320
Qy 301 VKSCSHLNKKTGMWFMNCGLANLNGIHHSFSGKLATGIGMGTWTKNNSPVKIKSVSMKIR 360
Db 321 VKSCSHLNKKTGMWFMNCGLANLNGIHHSFSGKLATGIGMGTWTKNNSPVKIKSVSMKIR 380
Qy 361 RMYNPFYK 368
Db 381 RMYNPFYK 388

RESULT 5
AAB82593
ID AAB82593 standard; Protein; 306 AA.
XX
AC AAB82593;
XX
DT 02-OCT-2001 (first entry)
XX
DE Human prothrombinase-like polypeptide splice variant mature protein.
XX
KW Prothrombinase-like polypeptide; human; haemostatic; cardiac;
KM nephrotropic; antidiabetic; hepatotropic; antiviral; cytostatic;
KM antiarteriosclerotic; antiulcer; vulnerary; osteoporosis;
KW immunomodulatory; antirheumatic; antiarthritic; antiinflammatory;
KM thrombolytic; diagnosis; therapy.
XX
OS Homo sapiens.
XX
PN WO200153456-A2.
XX
PD 26-JUL-2001.
XX
PF 22-DEC-2000; 2000WO-US35061.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-JAN-2000; 2000US-0491404.
PR 25-APR-2000; 2000US-0552317.
PR 17-JUN-2000; 2000US-0596196.
PR 31-AUG-2000; 2000US-0643313.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
PI Arterburn MC, Tang YT, Liu C, Drmanac R;
XX
DR WPI: 2001-483140/52.
DR N-PSDB; AAH26237.
XX
PT Novel prothrombinase-like polypeptides and polynucleotides useful in
PT diagnosing and treating e.g. myocardial infarction and diabetes -
PS Claim 10; Page 135-136; 140pp; English.
XX
CC The present sequence is that of the mature portion of a novel
CC secreted, soluble splice variant (see AAB82590) of novel human
CC prothrombinase-like polypeptide (PVP). PVP polynucleotides and
CC polypeptides, including those comprising the mature protein of the
CC PVP splice variant, can be used in the diagnosis, treatment and/or
CC prevention of diseases associated with the dysregulation of
CC coagulation pathways, such as haemophilia, myocardial infarction,
CC glomerular disease, diabetes, fulminant viral hepatitis and
CC atherosclerosis. They may also be beneficial in the treatment of
CC viral infections and some forms of cancer. A claimed method of
CC treating a subject in need of enhanced PVP activity or expression
```

CC Involves the administration of PLP, a PLP agonist or a
CC polynucleotide encoding PLP. A claimed method of treating a subject
CC having need to inhibit activity or expression of PLP involves the
CC administration of a PLP antagonist, a polynucleotide that inhibits
CC expression of a PLP polynucleotide, or a polypeptide that competes
CC with the PLP for its ligand. The polypeptides can also be used to
CC raise antibodies, as food supplements, and to screen for agonists
CC and antagonists.

XX Sequence 306 AA;

Query Match 81.2%; Score 1625; DB 22; Length 306;
Best Local Similarity 83.2%; Pred. No. 3e-157; Indels 62; Gaps 1;
Matches 306; Conservative 0; Mismatches 0;

QY 1 EVVQNCVHSTDSVYNIYEDGSNAKDESKNDYCKEDCEESCDYKTKITREKHFMC 60
DB 1 EVVQNCVHSTDSVYNIYEDGSNAKDESKNDYCKEDCEESCDYKTKITREKHFMC 60
QY 61 RNLQNSIVSYTRSTKLLRNMDQOASLDYLSNQVNELMNRVLLTTEVFRKQLDPPH 120
DB 61 RNLQNSIVSYTRSTKLLRNMDQOASLDYLSNQVNELMNRVLLTTEVFRKQLDPPH 120
QY 121 RPVQSHGLDCTDKDTIGSTKTPSGLYIHPBESSYFEVCMCDMDYRGCGWTYQKRID 180
DB 121 RPVQSHGLDCTDKDTIGSTKTPSGLYIHPBESSYFEVCMCDMDYRGCGWTYQKRID 180
QY 181 GIIDFQRLMCDYLDGFDLGEFMLGLKIFLYNQKNTSPMLVYALESEDDTLAYASYD 240
DB 181 GIIDFQRLMCDYLDGFDLGEFMLGLKIFLYNQKNTSPMLVYALESEDDTLAYASYD 240
QY 241 NFWLEDETRFPMKHLGRYSNAGDAFRLKREDNQNAMPESTSDVNDGCRPACTVNGQS 300
DB 241 NFWLEDETRFPMKHLGRYSNAGDAFRLKREDNQNAMPESTSDVNDGCRPACTVNGQS 300
QY 301 VKSCSHLHNTGWFNECGLANLNGIHFSCKLATGIONGTWTKNNSPVKIKSVSMKIR 360
DB 301 VKSCSHLHNTGWFNECGLANLNGIHFSCKLATGIONGTWTKNNSPVKIKSVSMKIR 360
QY 361 RMTNPFYK 368
DB 361 RMTNPFYK 368

RESULT 6
AAU14275
AAU14275 standard; protein; 326 AA.

XX AAU14275;
XX 24-OCT-2001 (first entry)
XX Human novel protein #146.
XX Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
XX Immunomodulatory; cytosolic; neuroprotective; vulnerrary; noctropic;
XX anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
XX antibacterial; antiallergic; dermatoprotective; haemostatic; antiasthmatic;
XX thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
XX Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
XX tissue regeneration; immune disorder.
XX Homo sapiens.
XX OS
XX PN WO200155437-A2.
XX PD 02-AUG-2001.
XX 25-JAN-2001; 2001WO-US02623.
XX 25-JAN-2000; 2000US-0491404.
XX (HYSE-) HYSEQ INC.
XX PA

XX Tang YT, Liu C, Drmanac RT;
XX WPI: 2001-451939/48.
XX DR N-PSDB; AAS22580.
XX
XX Isolated polypeptides useful for treating anti-inflammatory diseases,
XX nervous system disorders, and for regenerating bone and cartilage -
XX
XX Example 4; Page 605; 894pp; English.

CC The invention relates to polynucleotides encoding novel human
CC proteins or their active domains. The polypeptides, polynucleotides and
CC antibodies raised against the polypeptides are used in a method of
CC treatment of a mammal and prevention of disorders caused by the aberrant
CC protein expression or activity. The polypeptides can be used as
CC molecular weight markers, food supplements, and in antibody production.
CC The polypeptides are used to identify compounds which bind to the
CC polypeptides. Polynucleotides of the invention are used as probes and
CC primers, for sequencing, for chromosome or gene mapping, in the
CC production of recombinant proteins, and in generating anti-sense DNA or
CC RNA and in gene therapy. Polypeptides of the invention can be used to
CC target drugs to a tumour, in assays to determine biological activity, to
CC raise antibodies/elicite an immune response, to determine quantitative
CC protein levels, as tissue markers, and to isolate receptors or ligands.
CC Polypeptides of the invention may also be useful in treating platelet
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC ligament and/or nerve tissue, wound healing, treating burns, promoting
CC the proliferation, differentiation and survival of stem cells, as a
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC fungal infection or from autoimmunity, cancer, allergy, asthma,
CC graft-versus-host disease, eczema, haemophilia, thrombosis,
CC anti-inflammatory diseases, nervous system disorders, and infection.
CC The present sequence represents a protein of the invention.

XX Sequence 326 AA;

Query Match 81.2%; Score 1625; DB 22; Length 326;
Best Local Similarity 83.2%; Pred. No. 3.3e-157; Indels 62; Gaps 1;
Matches 306; Conservative 0; Mismatches 0;

QY 1 EVVQNCVHSTDSVYNIYEDGSNAKDESKNDYCKEDCEESCDYKTKITREKHFMC 60
DB 1 EVVQNCVHSTDSVYNIYEDGSNAKDESKNDYCKEDCEESCDYKTKITREKHFMC 80
QY 61 RNLQNSIVSYTRSTKLLRNMDQOASLDYLSNQVNELMNRVLLTTEVFRKQLDPPH 120
DB 61 RNLQNSIVSYTRSTKLLRNMDQOASLDYLSNQVNELMNRVLLTTEVFRKQLDPPH 140
QY 121 RPVQSHGLDCTDKDTIGSTKTPSGLYIHPBESSYFEVCMCDMDYRGCGWTYQKRID 180
DB 121 RPVQSHGLDCTDKDTIGSTKTPSGLYIHPBESSYFEVCMCDMDYRGCGWTYQKRID 200
QY 181 GIIDFQRLMCDYLDGFDLGEFMLGLKIFLYNQKNTSPMLVYALESEDDTLAYASYD 240
DB 181 GIIDFQRLMCDYLDGFDLGEFMLGLKIFLYNQKNTSPMLVYALESEDDTLAYASYD 220
QY 241 NFWLEDETRFPMKHLGRYSNAGDAFRLKREDNQNAMPESTSDVNDGCRPACTVNGQS 300
DB 241 NFWLEDETRFPMKHLGRYSNAGDAFRLKREDNQNAMPESTSDVNDGCRPACTVNGQS 258
QY 301 VKSCSHLHNTGWFNECGLANLNGIHFSCKLATGIONGTWTKNNSPVKIKSVSMKIR 360
DB 301 VKSCSHLHNTGWFNECGLANLNGIHFSCKLATGIONGTWTKNNSPVKIKSVSMKIR 318
QY 361 RMTNPFYK 368
DB 361 RMTNPFYK 326

RESULT 7

AAU14511
ID AAU14511 standard; Protein: 326 AA.
XX
AC AAU14511;
XX
DT 24-OCT-2001 (first entry).
XX
DE Human novel protein #382.
XX
KW Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW Immunomodulatory; cytostatic; neuroprotective; vulnerrary; neotrophic;
KW anticonvulsant; antiallergic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antilepteric; dermatological; haemostatic; antiaslomatic;
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX
OS Homo sapiens.
XX
PN WO200155437-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02623.
XX
PR 25-JAN-2000; 2000US-0491404.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI: 2001-451939/48.
DR N-PSDB: AAS22816.
XX
PT Isolated polypeptides useful for treating anti-inflammatory diseases,
PT nervous system disorders, and for regenerating bone and cartilage -
XX
PS Example 4; Page 848-849; 894pp; English.
XX
XX The invention relates to polynucleotides encoding novel human
XX proteins or their active domains. The polypeptides, polynucleotides and
XX antibodies raised against the polypeptides are used in a method of
XX treatment of a mammal and prevention of disorders caused by the aberrant
XX protein expression or activity. The polypeptides can be used as
XX molecular weight markers, food supplements, and in antibody production.
XX The polypeptides are used to identify compounds which bind to the
XX primers, for sequencing, for chromosome or gene mapping, in the
XX production of recombinant proteins, and in generating anti-sense DNA or
XX RNA and in gene therapy. Polypeptides of the invention can be used to
XX target drugs to a tumour, in assays to determine biological activity, to
XX raise antibodies/elicite an immune response, to determine quantitative
XX protein levels, as tissue markers, and to isolate receptors or ligands.
XX Polypeptides of the invention may also be useful in treating platelet
XX disorders, stem cell disorders, regenerating bone, cartilage, tendon,
XX ligament and/or nerve tissue, wound healing, treating burns, promoting
XX the proliferation, differentiation and survival of stem cells, as a
XX contraceptive, treating osteoporosis and osteoarthritis, anaemia,
XX Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
XX sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
XX fungal infection or from autoimmunity, cancer, allergy, asthma,
XX anti-infectious diseases, eczema, haemophilia, thrombosis,
XX anti-inflammatory diseases, nervous system disorders, and infection.
XX The present sequence represents a protein of the invention.
SQ Sequence 326 AA;
Query Match 81.2%; Score 1625; DB 22; Length 326;
Best Local Similarity 83.2%; Pred. No. 3.3e-157;
Matches 306; Conservative 0; Mismatches 0; Indels 62; Gaps 1;
QY 1 EVVQNCVHSHSTDSVYVIVEDGSAKDESKSNDTVCKEDCESCDVTKITREKHPMC 60
|||||

DB 21 EVVQNCVHSHSTDSVYVIVEDGSAKDESKSNDTVCKEDCESCDVTKITREKHPMC 80
QY 61 RNLQNSIVSYSTSTKLLNNMDEQASLDYLSNOVNEIMANRVLLTTEVERKQDPEPH 120
DB 81 RNLQNSIVSYSTSTKLLNNMDEQASLDYLSNOVNEIMANRVLLTTEVERKQDPEPH 140
QY 121 RPOVSHGLDCTDIDKPTIGSVTKTPSGLYTHPEGSSYPEVWCMDYRGCGWTVLOKRID 180
DB 141 RPOVSHGLDCTDIDKPTIGSVTKTPSGLYTHPEGSSYPEVWCMDYRGCGWTVLOKRID 200
QY 181 GIIDFQRLMCDYLDGFGDLDGEFWLGLKRFYIVNQKNTSFMLYALASEDDTLVASYD 240
DB 201 GIIDFQRLMCDYLDGFGDLDGEFWLGLKRFYIVNQKNTSFMLYALASEDDTLVASYD 220
QY 241 NFWLEDETRFEKMLHGRYSGNAGDAFRGLKKEDNDNAMPSTSDVNDGCRPACLVNGQS 300
DB 221 -----GDAFRGLKKEDNDNAMPSTSDVNDGCRPACLVNGQS 258
QY 301 VKSCSHLHNTGTGMPNECGLANLNGIHFSGLKLTATGLOWGTWTKNSPVKIKSYMKIR 360
DB 259 VKSCSHLHNTGTGMPNECGLANLNGIHFSGLKLTATGLOWGTWTKNSPVKIKSYMKIR 318
QY 361 RMYNPFYK 368
DB 319 RMYNPFYK 326
RESULT 8
AAB82590
ID AAB82590 standard; Protein: 326 AA.
XX
AC AAB82590;
XX
DT 02-OCT-2001 (first entry)
XX
DE Human prothrombinase-like polypeptide splice variant.
XX
KW Prothrombinase-like polypeptide; human; haemostatic; cardiant;
KW nephrotropic; antidiabetic; hepatotropic; antiviral; cytostatic;
KW antileukosclerotic; antitumor; vulnerrary; osteoporosis;
KW immunomodulatory; antipneumatic; antiallergic; antiinflammatory;
KW thrombolytic; diagnosis; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= "Signal peptide
FT /note= "separately claimed in Claim 10"
FT Protein 21..326
FT /label= "Mature protein
FT /note= "separately claimed in Claim 10"
FT Domain 181..217
FT /note= "fibrinogen beta/gamma chain"
FT Domain 262..292
FT /note= "fibrinogen beta/gamma chain"
FT Domain 82..321
FT /note= "blood coagulation domain, separately
FT claimed in Claim 10"
XX
XX WO200153456-A2.
PD 26-JUL-2001.
XX
XX 22-DEC-2000; 2000WO-US35061.
XX
XX 21-JAN-2000; 2000US-0488725.
XX 25-JAN-2000; 2000US-0491404.
XX 25-APR-2000; 2000US-0552317.
XX 17-JUN-2000; 2000US-0596196.
XX 31-AUG-2000; 2000US-0643313.
PA (HYSE-) HYSEQ INC.

XX Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
 PI Arterburn MC, Tang YT, Liu C, Dirmanac R;
 XX
 DR WPI: 2001-483140/52.
 DR N-PSDB: AAR26237.
 PT Novel prothrombinase-like polypeptides and polynucleotides useful in
 XX diagnosing and treating e.g. myocardial infarction and diabetes -
 PS Claim 10: Page 133; 140pp: English.
 XX
 CC The present sequence is that of a secreted, soluble splice variant
 CC of novel human secreted prothrombinase-like polypeptide (PLP, see
 CC also AAR26237). The splice variant has a predicted mol. wt. of
 CC 37,000 (unglycosylated) and shows amino acid sequence similarity to
 CC human prothrombinase Fg12 protein. The sequence was predicted from
 CC a polynucleotide (see AAR26237) derived from a human ovary cDNA
 CC comprising the mature protein, signal peptide or blood coagulation
 CC domain of the splice variant, can be used in the diagnosis,
 CC treatment and/or prevention of diseases associated with the
 CC dysregulation of coagulation pathways, such as haemophilia
 CC myocardial infarction, glomerular disease, diabetes, fulminant viral
 CC hepatitis and atherosclerosis. They may also be beneficial in the
 CC treatment of viral infections and some forms of cancer. A claimed
 CC method of treating a subject in need of enhanced PLP activity or
 CC expression involves the administration of PLP, a PLP agonist or a
 CC polynucleotide encoding PLP. A claimed method of treating a subject
 CC having need to inhibit activity or expression of PLP involves the
 CC administration of a PLP antagonist, a polynucleotide that inhibits
 CC expression of a PLP polynucleotide, or a polypeptide that competes
 CC with the PLP for its ligand. The polypeptides can also be used to
 CC raise antibodies, as food supplements, and to screen for agonists
 CC and antagonists.
 CC
 XX
 SQ Sequence 326 AA:
 Query Match 81.2%; Score 1625; DB 22; Length 326;
 Best Local Similarity 83.2%; Pred. No. 3.3e-157;
 Matches 306; Conservative 0; Mismatches 0; Indels 62; Gaps 1;

ID ABP51422 standard; Protein; 335 AA.
 XX
 AC ABP51422;
 XX
 DT 03-SEP-2002 (first entry)
 XX
 DE Human MDDR SEQ ID NO 444.
 XX
 KW Human; MDDR: disease detection and treatment molecule polynucleotide;
 KW proliferative disorder; hepatitis; psoriasis; cancer; AIDS;
 KW autoimmune disorder; inflammatory disorder; allergy; multiple sclerosis;
 KW rheumatoid arthritis; transgenic; gene therapy; antihistaminic;
 KW hepatotropic; antiinflammatory; antipsoriatic; cytostatic; anti-HIV;
 KW antiallergic; antianaemic; antiasthmatic; antiatherosclerotic; angiot;
 KW neuroprotective; antirheumatic; antiarthritic.
 XX
 OS Homo sapiens.
 XX
 PN MO200240715-A2.
 XX
 PD 23-MAY-2002.
 XX
 PF 06-SEP-2001; 2001WO-US27628.
 XX
 PR 06-SEP-2000; 2000US-230505P.
 PR 06-SEP-2000; 2000US-230514P.
 PR 06-SEP-2000; 2000US-230515P.
 PR 06-SEP-2000; 2000US-230517P.
 PR 06-SEP-2000; 2000US-230518P.
 PR 06-SEP-2000; 2000US-230519P.
 PR 06-SEP-2000; 2000US-230595P.
 PR 06-SEP-2000; 2000US-230597P.
 PR 06-SEP-2000; 2000US-230598P.
 PR 06-SEP-2000; 2000US-230599P.
 PR 06-SEP-2000; 2000US-230610P.
 PR 06-SEP-2000; 2000US-230655P.
 PR 06-SEP-2000; 2000US-230988P.
 PR 06-SEP-2000; 2000US-230989P.
 PR 07-SEP-2000; 2000US-230951P.
 PR 07-SEP-2000; 2000US-231163P.
 PR 07-SEP-2000; 2000US-231167P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Jackson S, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL;
 PI Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR;
 PI Momiya MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM;
 PI Gerstin EH, Peralta CH, David WH, Panzer SR, Flores V, Delfo A;
 PI Marwaha R, Chen AJ, Chang SC, Au AP, Imman RR;
 XX
 DR WPI: 2002-527544/56.
 DR N-PSDB: ABQ72639.
 XX
 PT Novel human disease detection and treatment polypeptide, useful in
 PT diagnosis, prevention or treatment of cell proliferative disorders e.g.
 PT arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder
 PT e.g. AIDS -
 XX
 PS Claim 14: Page 576-577; 618pp: English.
 XX
 CC The invention relates to an isolated human disease detection and
 CC treatment (MDDR) polypeptide (I) selected from a polypeptide having a
 CC sequence selected from 254 sequences (ABP51231-ABP51484) given in the
 CC specification, a naturally occurring polypeptide comprising a sequence
 CC having at least 90% identity to (I) or a biologically active or
 CC immunogenic fragment of (I). (I) is useful for screening a compound for
 CC effectiveness as an agonist or antagonist, for screening a compound that
 CC specifically binds (I) or modulates the activity of (I), and for
 CC preparing a polyclonal or monoclonal antibody by hybridoma technology.
 CC Nucleic acids (II) (ABQ72449-ABQ72700) encoding (I) are useful for
 CC screening a compound for effectiveness in altering expression of a target
 CC polynucleotide comprising. Oligonucleotides and antibodies are useful for
 CC detecting MDDR in a sample or for assessing toxicity of a test compound,

RESULT 11
AAB82592 standard; Protein: 240 AA.
XX
AC AAB82592:
XX
DT 02-OCT-2001 (first entry)
XX
DE Human prothrombinase-like polypeptide splice variant domain.
XX
KW Prothrombinase-like polypeptide: human; haemostatic; cardiac;
KW nephrotropic; antidiabetic; hepatotropic; antiviral; cytostatic;
KW antiarteriosclerotic; antiulcer; vulnery; osteoporosis;
KW immunomodulatory; antirheumatic; antiarthritic; antiinflammatory;
KW thrombolytic; diagnosis; therapy; blood coagulation.
XX
OS Homo sapiens.
XX
PN WO200153456-A2.
XX
PD 26-JUL-2001.
XX
PF 22-DEC-2000; 2000WO-US35061.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-JAN-2000; 2000US-0491404.
PR 25-APR-2000; 2000US-0552317.
PR 17-JUN-2000; 2000US-0596196.
PR 31-AUG-2000; 2000US-0643313.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
PI Arterburn MC, Tang YT, Liu C, Drmanac R;
XX
DR WPI: 2001-483140/52.
DR N-PSDB; AAB82592.
XX
PT Novel prothrombinase-like polypeptides and polynucleotides useful in
PT diagnosing and treating e.g. myocardial infarction and diabetes -
XX
PS Claim 10; Page 134-135; 140pp; English.
XX
CC The present sequence is that of the blood coagulation domain of a
CC secreted, soluble splice variant (see AAB82590) of novel human
CC prothrombinase-like polypeptide (PLP). PLP polynucleotides and
CC polypeptides, including those comprising the present domain of the
CC PLP splice variant, can be used in the diagnosis, treatment and/or
CC prevention of diseases associated with the dysregulation of
CC coagulation pathways, such as haemophilia, myocardial infarction,
CC glomerular disease, diabetes, fulminant viral hepatitis and
CC atherosclerosis. They may also be beneficial in the treatment of
CC viral infections and some forms of cancer. A claimed method of
CC treating a subject in need of enhanced PLP activity or expression
CC involves the administration of PLP, a PLP agonist or a
CC polynucleotide encoding PLP. A claimed method of treating a subject
CC having need to inhibit activity or expression of PLP involves the
CC administration of a PLP antagonist, a polynucleotide that inhibits
CC expression of a PLP polynucleotide, or a polypeptide that competes
CC with the PLP for its ligand. The polypeptides can also be used to
CC raise antibodies, as food supplements, and to screen for agonists
CC and antagonists.
XX
SQ Sequence 240 AA;
XX
Query Match 63.2%; Score 1265; DB 22; Length 240;
Best Local Similarity 79.5%; Pred. No. 1.3e-10;
Matches 240; Conservative 0; Mismatches 0; Indels 62; Gaps 1;
OY 62 NLQNSIVYSTRSTKRLKLNMDDEQASLDYLSNOVNEIMNRYLLTTEVFRKQDLPFPHR 121
DB 1 NLQNSIVYSTRSTKRLKLNMDDEQASLDYLSNOVNEIMNRYLLTTEVFRKQDLPFPHR 60

OY 122 PVQSHGLDCTDIDKDTIGSVTKTPSGLYTIHPEGSSYPPEVNCMDMDYRGCGMTVIQKRIDG 181
DB 61 PVQSHGLDCTDIDKDTIGSVTKTPSGLYTIHPEGSSYPPEVNCMDMDYRGCGMTVIQKRIDG 120
OY 182 IIDFQRLMCDYLDGFGDLDGFEWGLKRIYIVQKNKSPMLVYALASEDDTLAYASIDN 241
DB 121 IIDFQRLMCDYLDGFGDLDGFEWGLKRIYIVQKNKSPMLVYALASEDDTLAYASIDN 139
OY 242 FWLEDETRFFKMHILGRYSNAGDAFRGLKKEEDNQNAMPSTSDVNDGCRPACLVNGOSV 301
DB 140 -----GDAFRGLKKEEDNQNAMPSTSDVNDGCRPACLVNGOSV 178
OY 302 KCSHLHNKGTGWFEWNECGLANLNGIHFSGKILATGIQMGWTNKNKSPVKIKYSMKIRR 361
DB 179 KCSHLHNKGTGWFEWNECGLANLNGIHFSGKILATGIQMGWTNKNKSPVKIKYSMKIRR 238
OY 362 MY 363
DB 239 MY 240
RESULT 12
ABG22365
ID ABG22365 standard; Protein: 141 AA.
XX
AC ABG22365;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #22356.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PR 30-MAR-2001; 2001WO-US08631.
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR N-PSDB; AAB86552.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 52724; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations

PS Claim 20; SEQ ID No 52723; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

SO Sequence 116 AA;

Query Match 26.1%; Score 521; DB 22; Length 116;
Best Local Similarity 93.1%; Pred. No. 4.6e-45;
Matches 95; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 141 TKTPSGIYIHPRGSSYFEVCMCDYRGCGWYIQKRIGIIDFORLWCDYLDGFDLL 200
DB 13 TKTPSGIYIHPRGSSYFEVCMCDYRGCGWYIQKRIGIIDFORLWSDYLDGFDLV 72
OY 201 GEFWLGKRIFFIYNOKNTSEFNLVALESDDTLAYSYDNF 242
DB 73 GEFWLGKRIFFIYNOKNTSEFNLVALESDDTLAYSYDNF 114

RESULT 15

AAV26196
ID AAV26196 standard; protein; 491 AA.

AC AAV26196;

XX 03-NOV-1999 (first entry)

DE Human zapo3 protein.

XX Human zapo3 protein; angiotensin-1; angiotensin-2; covalently linked;
KW moiety; affinity tag; toxin; radionuclide; enzyme; fluorophore; multimer;
KW coiled coil domain; carboxyl-terminal fibrinogen-like domain; angiotensin;
KW haematopoietic; mitogenic activity; angiogenesis; inhibitor;
KW endocrine-vascular cell association; revascularisation; DNA probe;
KW neuronal degeneration; anti-zapo3 antibody.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..21

FT Peptide /label= Secretory_Signal_Sequence

FT Peptide 43..48

FT Peptide /label= Immunogen

FT Peptide /note= "For production of antibodies"

FT Peptide 93..98

FT Peptide /label= Immunogen

FT Peptide /note= "For production of antibodies"

FT Peptide 120..125

FT Peptide /label= Immunogen

FT Peptide /note= "For production of antibodies"

FT Peptide 421..426

FT Peptide /label= Immunogen

FT Peptide /note= "For production of antibodies"

FT Peptide 422..427

FT /label= Immunogen

FT /note= "For production of antibodies"

FT Domain 279..490

FT /label= Fibrinogen-like domain

FT /note= "Homologous to residues 631-864 of human
fibrinogen alpha chain"

FT Domain 63..253

FT /label= Amino-terminal_coiled_coil_domain

FT MISC-difference 280

FT /note= "Conserved cysteine residue"

FT MISC-difference 309

FT /note= "Conserved cysteine residue"

FT MISC-difference 432

FT /note= "Conserved cysteine residue"

FT MISC-difference 445

FT /note= "Conserved cysteine residue"

XX WO940193-A1.

XX 12-AUG-1999.

XX 03-FEB-1999; 99WO-US02303.

XX 04-FEB-1998; 98US-0018258.

XX (ZYMO) ZYMOGENETICS INC.

XX Holloway JL, Shoemaker KE;

XX WPI; 1999-508503/42.

XX N-PSDB; AAX80866.

PT Human angiotensin homologue, ZAPo3 useful for study and regulation

PS Claim 1; Page 65-67; 78pp; English.

XX The present sequence is a human zapo3 protein. Zapo3 protein exhibits
CC significant amino acid sequence homology to angiotensin-1 and 2. It is
CC covalently linked to a moiety chosen from affinity tags, toxins,
CC radionuclides, enzymes and fluorophores. The protein is assembled as a
CC multimer and is characterized by an amino-terminal coiled coil domain and
CC a carboxyl-terminal fibrinogen-like domain. Zapo3 has angiogenic,
CC haematopoietic and mitogenic activity. It is useful in the study and
CC regulation of angiogenesis, and for developing inhibitors of
CC angiogenesis. It is possibly involved in modulation of endocrine-vascular
CC cell association and may be used therapeutically to stimulate the
CC revascularisation of tissue, to promote angiogenesis and prevent neuronal
CC degeneration. DNA probes and anti-zapo3 antibodies can be used to detect
CC sites of angiogenesis.

SO Sequence 491 AA;

Query Match 21.2%; Score 425; DB 20; Length 491;
Best Local Similarity 26.9%; Pred. No. 2.7e-34;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

OY 24 SNAKDESKNDYVCKECCESCQYKKTIRE-EKHFKRNLQNSIYSTSTKLRLNM 82

DB 68 TKGDASTIRDMTRMDLNLKIDVLSKQREIDVQLVVDGNIVNEVLRKESHNM 127

OY 83 DE-QQASLDYV-----SNQVNEAMNVLTLTE----- 109

DB 128 SRVQLYMOQLHEIRKRDNSLEISQLEKILAVTTMLMATRYRELEVKASLDLVN 187

OY 110 -----VFRKO--LDP-----FPHRPVQSHGL----- 128

DB 188 NOSVMITLBEQCLIRPSRQDTHVSPPLVQVPOHINSGQYVPGLLGNGEIQRDGPR 247

OY 129 DCYDIKDTISVYKTP-----SGLYIHPRGSSYFEV 161

DB 248 DLMPPLATSPKSPKIPPTVFINEGPKDCQAKGASHVSGLYIMIPENSNGMOL 307

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 16, 2002, 17:32:58 ; Search time 15.3968 Seconds
(without alignments)
2422.587 Million cell updates/sec

Title: US-09-596-196-4

Perfect score: 2104
Sequence: 1 NMSPSQASLLFLNVCIFIG.....PVKIKSVSMKIRMYNPPRK 388

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:***
1: PIR1:***
2: PIR2:***
3: PIR3:***
4: PIR4:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	413.5	19.7	439	2 I37391	fibrinogen-like pr
2	405.5	19.3	432	2 A27447	cytotoxic T-lympho
3	401.5	19.1	432	2 I56934	fibrinogen-like pr
4	397	18.9	312	2 JN0596	fibrinogen-related
5	394.5	18.8	468	1 FGB0B	fibrinogen beta ch
6	375.5	17.8	491	1 FGH0B	fibrinogen beta ch
7	371.5	17.7	437	1 FGH0B	fibrinogen beta ch
8	371.5	17.7	453	1 FGH0B	fibrinogen beta ch
9	371.5	17.7	463	1 FGH0B	fibrinogen beta ch
10	370	17.6	479	2 A25052	fibrinogen beta ch
11	365	17.3	444	2 S05313	fibrinogen gamma-B
12	363	17.3	432	2 FGLMS	fibrinogen gamma-B
13	353	16.8	438	2 A32670	fibrinogen gamma c
14	350.5	16.7	282	2 A35084	fibrinogen-related
15	348.5	16.6	774	2 A39832	scabrous locus (sc
16	346.5	16.5	328	2 A05299	fibrinogen beta ch
17	337.5	16.0	866	2 D44234	fibrinogen alpha c
18	330	15.7	1356	2 A45445	janusin precursor,
19	329	15.6	334	2 JC5980	fibronectin alpha-I
20	328.5	15.6	641	1 A41932	fibronectin alpha-I
21	327.5	15.6	1353	2 JH0675	transforming growt
22	312	14.8	323	2 A47172	transforming growt
23	311.5	14.8	437	1 FGR7GA	fibrinogen gamma-A
24	311.5	14.8	445	1 FGR7GA	fibrinogen gamma-B
25	310.5	14.8	4135	2 T42629	tenascin-X - bovin
26	310.5	14.8	1810	1 A32230	tenascin precursor
27	304.5	14.5	1914	2 T42635	tenascin Y precurs
28	303.5	14.4	326	2 S61517	tenascin-1 precurs
29	302.5	14.4	3566	1 A40701	tenascin-X precurs

30	299	14.2	417	2 S65944	tenascin-X - pig (
31	296	14.1	220	2 S28170	tenascin homolog -
32	295	14.0	326	2 B47172	tenascin-beta - pig
33	286	13.6	860	2 I48839	tenascin-X - mouse
34	284.5	13.5	2019	1 J01322	tenascin precursor
35	283.5	13.5	4006	2 T09070	probable tenascin
36	282.5	13.4	1746	1 S19694	tenascin precursor
37	271	12.9	2201	2 A32160	tenascin-C - human
38	212.5	10.1	463	2 T15876	hypothetical prote
39	180.5	8.6	915	2 T21773	hypothetical prote
40	180.5	8.6	927	2 T21772	hypothetical prote
41	173	8.2	431	2 T29850	hypothetical prote
42	154.5	7.3	933	2 A31930	cytotactin - chick
43	128.5	6.1	452	2 T26827	hypothetical prote
44	117	5.6	127	2 PC2036	microfibril-associ
45	110.5	5.3	4588	2 T28667	dynein beta heavy

ALIGNMENTS

RESULT 1
I37391
fibrinogen-like protein expressed in T lymphocytes (PI49) - human
C:Species: Homo sapiens (man)
C:Date: 01-Nov-1996 #sequence-revision 01-Nov-1996 #text-change 21-Jul-2000
C:Accession: I37391; S47273
R:Ruegg, R.
Gene 160, 257-262, 1995
A:Title: Sequence of a human transcript expressed in T-lymphocytes and encoding a fib
A:Reference number: I37391; MUID:95369700; PMID:7642106
A:Accession: I37391
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-439 <RES>
A:Cross-references: EMBL:Z26531; NID:9535184; PIDD:CA085298.1; PID:9535185
A:Note: Submitted to the EMBL Data Library, August 1994
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F;210-435/Domain: fibrinogen beta/gamma homology <FBG>

Query Match	19.7%	Score 413.5;	DB 2;	Length 439;
Best Local Similarity	30.2%	Pred. No. 8.6e-25;		
Matches 119;	Conservative 61;	Mismatches 147;	Indels 67;	Gaps 15;
QY	34	SSVNIYEDGSMNAKDESKNDYCKEDCE-----ESCQYKTK	70	
DB	73	SRIEVEKVEONLKEIYNLSKKSC-QDCKIADNDGDPGRNGLLPSTGAPGEYGDNRVR	131	
QY	71	ITREKHFMCNLTNS-----IVSYRSTKLLRNM-----MDEQASLDYLSNQVVELM	120	
DB	132	ELSEVKNKLSEELNAKEEIVLHGRLEKLNLYVMNNIENYVDSKVANLFFVNSLDGKC	191	
QY	121	NRVLLLTTEVFRKQLDPPHAPVOSHGL--DCTDIKRTIGSVKTPSGLYIIEGSSYP	178	
DB	192	SKC-----PSQEOIQSRVQ-HLIYKDCSDY---AIGRSSEIYKVPDPNNS	237	
QY	179	FEVNCDDYRGGWTVYIOKRIDGIIDFQRLMCDYLDGSGDLGFEWGLKPIFYVQNK	238	
DB	238	FEVYCDMEHMGWTVYQARLDGSTNFTKYQDYKAGFNIRREFWLGNDKIHLLT--KS	295	
QY	239	TSMFLYALAESEDDTLAYASYDNFMLEDETRFFFMHLYGRYSGNAGDAFRLKKEDNONAM	298	
DB	296	KEMILRIDLEDENFVCELYALDYQEVYANFELKYLHGVNNGTAGDALR-FNKHYNNDLK	354	
QY	299	PFSTSDVDNOCGRACLVNGSVKSCSHLNKTKTWMEGGLAUNG-IHFFSKLLATG	357	
DB	355	FTTPPDKDNDRYPSG-----NCG-LYSSGMPWDACLSANLNGKYYHOKYRGVRNG	404	
QY	358	IOMGTW--TKNNSPVKIKSVSMKIRRYNP-YFK	388	
DB	405	IFMGTWPGVSLAHGCGYKSSKEAKMMIRPKHF	438	

RESULT 2

A27447
cytotoxic T-lymphocyte-specific protein precursor (clone pT49) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 03-Dec-1999
C:Accession: A27447
R:Koyama, T.; Hall, L.R.; Haseg, W.G.; Toneyawa, S.; Salto, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 1609-1613, 1987
A:Title: Structure of a cytotoxic T-lymphocyte-specific gene shows a strong homology to
A:Reference number: A27447; MUID:8717527; PMID:3550794
A:Accession: A27447
A:Molecule type: mRNA
A:Residues: 1-432 <R>
A:Cross-references: GB:M16238; NID:g193304; PIDN:AAA37624.1; PID:g387156
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F:203-428/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 19.3%; Score 405.5; DB 2; Length 432;
Best Local Similarity 35.4%; Pred. No. 3.6e-24;
Matches 110; Conservative 43; Mismatches 115; Indels 43; Gaps 13;

QY 98 LNNMDEQA-----SLDLSNQVNELMNRVLLTTEVERKQD-----PPF 139

Db 137 LKNADQIOGLQRLLETLLVNMNIENYVDNRKANLTFVVV--NSLDGCKSPQSEHMQ 194

QY 140 HRPVSHGL--DCTDIKDTIGSVTTPSGLYTHHEGSSYPPEVWCDMDYRGGGTVIOK 197

Db 195 SOPVO-HLIYKDCSD-HYVLG---RRSSGAYRVTPDHRNSFEYVCDMETMGGGTVIOA 249

QY 198 RIDGIIDFQRLMCDYLDGFDLGEFWLGLKFIYVNOKNTPFMYLVASEDDTLAYA 257

Db 250 RLDGSTNFTREMKDYKAGFNGLEFELWGNKIHILT--KSEMLIRIDLEFNGILTLYA 307

QY 258 SYDNWLEDETRFFKMHILGRYSGNAGDAFRGLKEDNONAMPSTSDVNDGCRPACLVN 317

Db 308 LYDOFYVANEFLKYRLHIGNYNGTGDALR-PSRHYNHDLRFETTPDRNDYPSG---- 362

QY 318 GOSVSCSLHMKTKTGMWNEGCLANLNG-IHFGSKLATGOMGTWTKNN--SPVKIKS 374

Db 363 -----NCG-LYSSGWMWDSCLSANLNGKYHOKYKVRNGIFGTWPGINOAPGGYKS 416

QY 375 VSMKIRMYNP 385

Db 417 SFKQAKMIRP 427

RESULT 3

156934
fibrinogen-like protein - mouse
C:Species: Mus sp. (mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 03-Dec-1999
C:Accession: I56934
R:Patr, R.L.; Fung, L.; Reneker, J.; Myers-Mason, N.; Leibowitz, J.L.; Levy, G.
J. Virol. 69, 5033-5038, 1995
A:Title: Association of mouse fibrinogen-like protein with murine hepatitis virus induce
A:Reference number: I56934; MUID:95333285; PMID:7609073
A:Accession: I56934
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-432 <R>
A:Cross-references: GB:S78773; NID:g1042169; PIDN:AAB34823.1; PID:g1042170
C:Genetics:
A:Gene: mufib1p
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F:203-428/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 19.1%; Score 401.5; DB 2; Length 432;
Best Local Similarity 35.0%; Pred. No. 7.4e-24;
Matches 109; Conservative 43; Mismatches 116; Indels 43; Gaps 13;

QY 98 LNNMDEQA-----SLDLSNQVNELMNRVLLTTEVERKQD-----PPF 139

Db 137 LKNADQIOGLQRLLETLLVNMNIENYVDNRKANLTFVVV--NSLDGCKSPQSEHMQ 194

QY 140 HRPVSHGL--DCTDIKDTIGSVTTPSGLYTHHEGSSYPPEVWCDMDYRGGGTVIOK 197

Db 195 SOPVO-HLIYKDCSD-HYVLG---RRSSGAYRVTPDHRNSFEYVCDMETMGGGTVIOA 249

QY 198 RIDGIIDFQRLMCDYLDGFDLGEFWLGLKFIYVNOKNTPFMYLVASEDDTLAYA 257

Db 250 RLDGSTNFTREMKDYKAGFNGLEFELWGNKIHILT--KSEMLIRIDLEFNGILTLYA 307

QY 258 SYDNWLEDETRFFKMHILGRYSGNAGDAFRGLKEDNONAMPSTSDVNDGCRPACLVN 317

Db 308 LYDOFYVANEFLKYRLHIGNYNGTGDALR-PSRHYNHDLRFETTPDRNDYPSG---- 362

QY 318 GOSVSCSLHMKTKTGMWNEGCLANLNG-IHFGSKLATGOMGTWTKNN--SPVKIKS 374

Db 363 -----NCG-LYSSGWMWDSCLSANLNGKYHOKYKVRNGIFGTWPGINOAPGGYKS 416

QY 375 VSMKIRMYNP 385

Db 417 SFKQAKMIRP 427

RESULT 4

JN0596
fibrinogen-related protein HRP-1 precursor - human
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C:Accession: JN0596
R:Yamamoto, T.; Golch, M.; Sasaki, H.; Terada, M.; Kitajima, M.; Hirohashi, S.
Biochem. Biophys. Res. Commun. 193, 681-687, 1993
A:Title: Molecular cloning and initial characterization of a novel fibrinogen-related
A:Reference number: JN0596; MUID:95290661; PMID:8390249
A:Accession: JN0596
A:Molecule type: mRNA
A:Residues: 1-312 <Y>
A:Cross-references: GB:D14446; NID:g393314; PIDN:BA0336.1; PID:g393315
A:Experimental source: liver
C:Superfamily: fibrinogen beta/gamma homology
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-312/Product: fibrinogen-related protein HRP-1 #status predicted <MAT>
F:80-305/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 18.9%; Score 397; DB 2; Length 312;
Best Local Similarity 34.3%; Pred. No. 1.1e-23;
Matches 111; Conservative 44; Mismatches 115; Indels 54; Gaps 12;

QY 87 IVSYTRSTKLLRNMMDEQAISLDLSNQVNELMNRVLLTTEVERKQ----- 134

Db 4 VPSFLVTVTALT---MGRISALDECAQOMRLRAQVRLLETRVQOQYKIKQLQENYV 60

QY 135 --LDPEPHRPVOSH-----LDCTDIKDTIGSVTTPSGLYTHHEGSSYPPEVWCDMDY 187

Db 61 QRLDGDEDETVVLDLSKROYADCEIFNDGYKL-----SGFYKIKPLQSPAFPSYVCDMS- 115

QY 188 RGGGTVIOKRIIDGIIDFQRLMCDYLDGFDL---GEWGLGLKFIYVNOKNTPFMY 244

Db 116 DGGGTVIOKRIIDGSENEFRGKWDYENGFGNFVQHGEXWLNKMLHFTTQED--YTLK 173

QY 245 VALESEDDTLAAYASDYNFLEDETRFFKMHILGRYSGNAGDAFRGLKEDN-----NAMP 299

Db 174 IDLAPEKRSRYAQYKRFVGDENKFEYELNIGYSGTADSLAGFHFPEVQWMAASHORRK 233

QY 300 FSTSDVNDGCRPACLVNGQSVKCSHLNKTGMWFNEGCLANLNGIHHFGSKLA--T 356

Db 234 FSTWDRDHNYEGNCAEEDS-----GWMFNCHSANLNGV--YISGPTAKTDN 281

QY 357 GTONGTWTKNNSPVAKISYMKIR 380

Db 282 GIVWYTW--HGWMYSIKSYVMKIR 303

RESULT 5

FCGBOB

[illegible][illegible]

A:Residues: 31-112, 'E', 114-137, 'Q', 140-144, 'Q', 147-148 <BLO>
 R:Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.
 Biochemistry 33, 1988-1993, 1994
 A:Title: Identification of proteins associated with apolipoprotein A-I-containing lipoproteins
 A:Reference number: A54223; MUID:94162201; PMID:8117655
 A:Accession: G54223
 A:Molecule type: protein
 A:Residues: 164-174 <RUN>
 A:Note: Identification of tryptic peptides from high-density lipoproteins
 R:Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.
 Ann. N. Y. Acad. Sci. 408, 28-43, 1983
 A:Title: Covalent structure of fibrinogen.
 A:Reference number: A90037; MUID:83254370; PMID:6575689
 A:Contents: annotation; review; disulfide bonds
 R:Gardlund, B.; Hessel, B.; Marguerie, G.; Morano, G.; Blomback, B.
 Eur. J. Biochem. 77, 595-610, 1977
 A:Title: Primary structure of human fibrinogen. Characterization of disulfide-containing
 A:Reference number: A91249; MUID:77245999; PMID:891553
 A:Contents: annotation; disulfide bonds
 R:Doollittle, R.F.; Takagi, T.; Matt, K.; Bouma III, H.; Cottrell, B.A.; Casaman, K.G.; G
 In Regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S., Ottesen, M., Folt
 A:Title: The structures of fibrinogen and fibrin.
 A:Reference number: A94437
 A:Contents: annotation; disulfide bonds
 R:Doollittle, R.F.
 Annu. Rev. Biochem. 53, 195-229, 1984
 A:Title: Fibrinogen and fibrin
 A:Reference number: A90041; MUID:84305751; PMID:6383194
 A:Contents: annotation; review, EM structure, polymerization, ligands
 R:Chung, D.W.; Rixon, M.W.; Que, B.G.; Davie, E.W.
 Ann. N. Y. Acad. Sci. 408, 449-456, 1983
 A:Title: Cloning of fibrinogen genes and their cDNA.
 A:Reference number: A90038; MUID:83254384; PMID:6575700
 A:Contents: annotation
 R:Kirschbaum, N.E.; Budzynski, A.Z.
 J. Biol. Chem. 265, 13669-13676, 1990
 A:Title: A unique proteolytic fragment of human fibrinogen containing the alpha COOH-ter
 A:Reference number: A37117; MUID:90337977; PMID:2143188
 A:Contents: annotation; hementin cleavage site
 A:Note: hementin, a protease from Haemertia phillipii, the giant South American leech,
 C:Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleave
 ization sites responsible for the formation of the soft clot.
 C:Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabiliz
 ger) and between alpha chains (weaker) of different monomers.
 C:Comment: All fibrinogen chains are synthesized in the liver.
 C:Genetics:
 A:Gene: GDB:FCB
 A:Cross-references: GDB:119130; OMIM:134830
 A:Map position: 4q28-4q28
 A:Introns: 38/3; 102/3; 164/1; 240/1; 278/1; 320/1; 415/2
 C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FC
 lns are contained in the core. Two three-chain coiled coils emerge from this core and co
 from the distal domain nodes.
 C:Function:
 A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
 A:Pathway: blood coagulation
 C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfid
 C:Keywords: blood coagulation; coiled coil; glycoprotein; liver; plasma; pyroglyutamic ac
 F:1-30/domain: (or 4-30 or 15-30) signal sequence #status predicted <SIG>
 F:31-49/Product: fibrinogen beta chain #status experimental <MAT>
 F:31-44/Product: fibrinopeptide B #status experimental <APT>
 F:45-49/Product: fibrin beta chain #status experimental <FGB>
 F:45-47/Region: polymerization site
 F:99-228/domain: fibrinogen disulfide ring homology <FDR>
 F:28-487/domain: fibrinogen beta/gamma homology <FBG>
 F:31/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
 F:44-45/Cleavage site: Arg-Gly (thrombin) #status experimental
 F:95/Disulfide bonds: interchain (to alpha-55) #status experimental
 F:106/Disulfide bonds: interchain (to alpha-68) #status experimental
 F:110/Disulfide bonds: interchain (to gamma-45) #status experimental
 F:223/Disulfide bonds: interchain (to alpha-184) #status experimental
 F:227/Disulfide bonds: interchain (to gamma-161) #status experimental
 F:231-316, 241-270, 424-437/Disulfide bonds: #status experimental

F:394/Binding site: carbohydrate (asn) (covalent) #status experimental
 Query Match 17.8%; Score 375.5; DB 1; Length 491;
 Best Local Similarity 26.6%; Pred. No. 9, 6e-22;
 Matches 118; Conservative 56; Mismatches 142; Indels 127; Gaps 17;
 QY 25 GNCVHSTDSVYNYVEDOSNAKDESKNDYCKEDCESCVKRTKEEHFMCNRQ 84
 DB 93 GGCLEHAPDLGLV-----CPTGCOLQELALQOE-----RPIR 124
 QY 85 NSI-----VSYTRSYK-----KLRRNMDQOASLDYLSNOYNELMN----- 121
 DB 125 NSYDELNNVNAVSGTSSSPQYMWILKDKMRKQKQVNDNENYNESELEKHQLYD 184
 QY 122 -----RVLLTTEVFRKKQDPP-----HRPVQSHGLDCTD 152
 DB 185 ETVNSNIPNLVLSLEENLRSKIOKLESDVSAQMEYCRPTGVSCNIPVVS -GKECE 243
 QY 153 IKDTIGSVTKPTSGLYIHDESSYPFEVPCMDYRGGWYIYQKRIGIIDFOLMCDY 212
 DB 244 IIRKGET-----SEWYLIQPDSSVPRVYCDMNTENGGMVLIQNRQDSYDFGRKMDPY 299
 QY 213 LDGFGD-----LLGEFWLGLKIFYIVQKNTSFMLYVLALESDDTLAVASYD 260
 DB 300 KGFQGVNATNDGKNVCGLPGEWLGNDKISQLTNRGPT-LLIEMEDMKDKYKAHNG 357
 QY 261 NWLEDETRFEFKMLGRSGNAGDAFRG---LKKEDN---ONAPSTSDVNDGCRP 312
 DB 358 GFYVNEAKYQIYSVYKTAGNALMDGASOLMKEENRTYIHNGMFEFTYDRDNG--- 414
 QY 313 ACLVNGQSVKSCSHLNKTKGMFNECGLANLNGIHHSKLT-----LATGIOMGYT 364
 DB 415 --WLTSDPRKQCK-EDGGGMWYNRCHAMPNGRYWGQYTMMAKHGTDDGVVMMW- 470
 QY 365 KNSPVKIKSVSMKIRMYNYPY 387
 DB 471 -KGSWYMKMKMKIR---PFF 488
 RESULT 7
 FGBUG
 fibrinogen gamma-A chain precursor [validated] - human
 N:Alternate names: coagulation factor I
 C:Species: Homo sapiens (man)
 C:Date: 24-Apr-1984 #sequence_revision 25-Feb-1985 #text_change 08-Dec-2000
 C:Accession: A90470; B90494; C94433; B93956; B92448; I37393; A40698; H54223; A03125;
 R:Chung, D.W.; Chan, W.Y.; Davie, E.W.
 Biochemistry 22, 3250-3256, 1983
 A:Title: Characterization of a complementary deoxyribonucleic acid coding for the gam
 A:Reference number: A90470; MUID:83283434; PMID:6686357
 A:Accession: A90470
 A:Molecule type: mRNA
 A:Residues: 1-437 <CHU>
 R:Rixon, M.W.; Chung, D.W.; Davie, E.W.
 Biochemistry 24, 2077-2086, 1985
 A:Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.
 A:Reference number: A90494; MUID:85252774; PMID:2990550
 A:Accession: B90494
 A:Molecule type: DNA
 A:Residues: 1-113, 'T', 115-437 <RTX>
 A:Cross-references: GB:X02415; GB:M10014; NID:g182438; PIDN:AB5531.1; PID:g182439
 R:Henschen, A.; Lottspeich, F.; Southan, C.; Topfer-Petersen, E.
 In Protides of the Biological Fluids, Proc. 28th Colloq., Peeters, H., ed., pp.51-56,
 A:Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structura
 A:Reference number: A94433
 A:Accession: C94433
 A:Molecule type: protein
 A:Residues: 27-437 <HEN>
 R:Kant, J.A.; Lord, S.T.; Crabtree, G.R.
 Proc. Natl. Acad. Sci. U.S.A. 80, 3953-3957, 1983
 A:Title: Partial mRNA sequences for human Aalpha, Bbeta, and gamma fibrinogen chains:
 A:Reference number: A93956; MUID:83247396; PMID:6575389
 A:Accession: B93956

A: Molecule type: mRNA
A: Residues: 276-437 <KAN>
R: Forrester, J., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.
J. Biol. Chem. 259, 12826-12830, 1984
A: Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near the
A: Reference number: A92448; PMID:85030379; PMID:6092346
A: Accession: B92448
A: Molecule type: DNA
A: Residues: 286-437 <FOR>
R: Riman, A.M.A.; Eaton, M.A.W.; Williamson, R.; Humphries, S.
Nucleic Acids Res. 11, 7427-7434, 1983
A: Title: Isolation and characterization of cDNA clones for the Aalpha- and gamma-chains
A: Reference number: 137393; PMID:84069777; PMID:6689067
A: Accession: 137393
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: mRNA
A: Residues: 209-270 <RES>
A: Cross-references: EMBL:X00086; NID:g31445; PIDN:CAA24944.1; PID:g577055
R: Bertagnoli, M.E.; Beckerle, M.C.
J. Cell Biol. 121, 1329-1342, 1993
A: Title: Evidence for the selective association of a subpopulation of GPIIb-IIIa with th
A: Reference number: A40698; PMID:93286185; PMID:8509453
A: Accession: A40698
A: Molecule type: protein
A: Residues: 27-33, 'XX', 36-41 <BER>
A: Experimental source: thrombin-activated platelets
A: Note: sequence extracted from NCBI backbone (NCBI:133734)
R: Luntlake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vlague, J.; Kane, J.P.
Biochemistry 33, 1988-1993, 1994
A: Title: Identification of proteins associated with apolipoprotein A-I-containing lipop
A: Reference number: A54223; PMID:94162201; PMID:8117655
A: Accession: H54223
A: Molecule type: protein
A: Residues: 27-33, 'XX', 36-41 <KUN>
A: Note: identification of tryptic peptides from high-density lipoproteins
R: Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.
Ann. N. Y. Acad. Sci. 408, 28-43, 1983
A: Title: Covalent structure of fibrinogen.
A: Reference number: A90037; PMID:83254370; PMID:6575689
A: Contents: annotation; review; disulfide bonds
R: Doolittle, R.F.; Takagi, T.; Matti, K.; Bouma III, H.; Cottrell, B.A.; Cassman, K.G.; G
in Regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S., Ottesen, M., Folt
A: Title: The structures of fibrinogen and fibrin.
A: Reference number: A94437
R: Blomback, B.; Hessel, B.; Hogg, D.
Thromb. Res. 8, 639-658, 1976
A: Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
A: Reference number: A94309; PMID:76225080; PMID:936108
A: Contents: annotation; disulfide bonds
R: Hoepflich, P.D.; Doolittle, R.F.
Biochemistry 22, 2049-2055, 1983
A: Title: Dimeric half-molecules of human fibrinogen are joined through disulfide bonds
A: Reference number: A90467; PMID:8321465; PMID:6660649
A: Contents: annotation; quaternary structure, disulfide bonds
R: Doolittle, R.F.
Annu. Rev. Biochem. 53, 195-229, 1984
A: Title: Fibrinogen and fibrin.
A: Reference number: A90041; PMID:84305751; PMID:6383194
A: Contents: annotation; review, EM structure, polymerization, ligands
R: Horvath, B.H.; Varadi, A.; Scheraga, H.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 5980-5984, 1984
A: Title: Localization of a fibrin gamma-chain polymerization site within segment Thr-374
A: Reference number: A94006; PMID:85014892; PMID:6592597
A: Contents: annotation; polymerization region
R: Kloczewiak, M.; Timmons, S.; Lukas, T.J.; Hawiger, J.
Biochemistry 23, 1767-1774, 1984
A: Title: Platelet receptor recognition site on human fibrinogen. Synthesis and structure
A: Reference number: A90483; PMID:84203545; PMID:6326808
A: Contents: annotation; platelet aggregation region
R: Plow, E.F.; Stouff, A.H.; Meyer, D.; Marguerie, G.; Ginsberg, M.H.
J. Biol. Chem. 259, 5388-5391, 1984
A: Title: Evidence that three adhesive proteins interact with a common recognition site o

A: Reference number: A92477; PMID:84185664; PMID:6325435
A: Contents: annotation; platelet aggregation region
R: Pang, C.V.; Ederly, R.F.; Bell, W.R.
J. Biol. Chem. 260, 9713-9719, 1985
A: Title: Localization of a fibrinogen calcium binding site between gamma-subunit post
A: Reference number: A92549; PMID:85261382; PMID:3160702
A: Accession: A92549
A: Contents: annotation; calcium binding region
R: Kirschbaum, N.E.; Budzynski, A.Z.
J. Biol. Chem. 265, 13669-13676, 1990
A: Title: A unique proteolytic fragment of human fibrinogen containing the Aalpha COOH
A: Reference number: A37117; PMID:90337977; PMID:2143188
A: Contents: annotation; hementin cleavage site
A: Note: hementin, a protease from Haemolysate gillaniti, the giant South American le
C: Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cle
ization sites responsible for the formation of the soft clot.
C: Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stab
ger) and between alpha chains (weaker) of different monomers.
C: Comment: All fibrinogen chains are synthesized in the liver.
C: Comment: The two forms of gamma chain, A and B (see PIR:FGHUB), arise by alternate
intron, which makes this chain different from the gamma-B chain at positions 434-437
A: Gene: FGG
A: Gene: FGG
A: Cross-references: GDB:119132; OMIM:134850
A: Map position: 4q28-4q28
A: Introns: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1; 433/3
C: Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR
ins are contained in the core. Two three-chain coiled coils emerge from this core and
from the distal domain nodes.
C: Function:
A: Description: fibrinogen cleaved by thrombin yields monomers that are polymerized in
A: Pathway: blood coagulation
C: Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C: Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprote
F: 1-26/Domain: signal sequence #status predicted <SIG>
F: 27-437/Product: fibrinogen gamma-A chain #status experimental <MRT>
F: 176-415/Domain: fibrinogen beta/gamma homology <RFG>
F: 341-355/Domain: calcium binding #status predicted <CAB>
F: 400-422/Region: polymerization site, binding to the amino end of the alpha chain of
F: 423-437/Region: platelet aggregation #status predicted
F: 34/Disulfide bonds: interchain (to gamma-35) #status experimental
F: 35/Disulfide bonds: interchain (to gamma-34) #status experimental
F: 45/Disulfide bonds: interchain (to beta-110) #status experimental
F: 49/Disulfide bonds: interchain (to alpha-64) #status experimental
F: 78/Binding site: carbohydrate (Asn) (covalent) #status experimental
F: 161/Disulfide bonds: interchain (to beta-227) #status experimental
F: 165/Disulfide bonds: interchain (to alpha-180) #status experimental
F: 179-208, 352-365/Disulfide bonds: #status experimental
F: 424/Cross-link: isopeptide (Gln) (interchain to Lys-432 N6-amino) #status experimen
F: 432/Cross-link: isopeptide (Lys) (interchain to Gln-424) #status experimental
Query Match 17.7% Score 371.5; DB 1; Length 437;
Best local similarity 31.9% Pred. No. 1,7e-21;
Matches 105; Conservative 42; Mismatches 129; Indels 53; Gaps 11;
OY 85 NSIVSYRSTRKLLRNMDQ-----QASIDVLSNOVNEMLRVLLLTVEFRKQDLP 138
DB 103 NMIDAATLKRKMLEIKYEASILTIDSSIRYQEIYNSNNGQIVMLKEV--AQLEAQ 160
OY 139 PHRP-----VQSH---GLDCDIDIKTIGSVYKTPBGLYIIIPBEGSYFPEWCDMDYDGGG 191
DB 161 CQEPCKDPTVOHDITGKDCD-----IANKGAKOGSLFIRPLKANOQFLVYCEIDGSGNG 216
OY 192 WTVQKRIIDGIDIPQRLMCDVLDGFDL---LQEFVGLKRIYIYNOKTSMVLVAL 247
DB 217 WTVQKRLDGSVDPKKMWIQYKEGFLHSPTGTETFLGNKRIHILISTQSAIPALVEL 276
OY 248 ESEDDTLAVASYDNFWMLEDTFRFKMLGRYS-GNADAFRGLKED-----NONAM 298
DB 277 EDWNGRSTADYAFKVGPEADKRYLTAYAFAGDADAEGFDGPDSPDKFTSHNG 336
OY 299 PFTSDVDNDCGRACLVNQGVSVCSSHLNKTQWMEVNEGLANLNIHRSGL----- 353
DB 337 QFTWDDNDNDQFEKNCABQDGS-----GMMNKKCHAGLNGVYVYOGGYSKAST 385

DB 386 PNGYDNGITMATW--KTRWYSMKTKTMTKI 412

RESULT 8
FCHUGH
fibrinogen gamma-B chain precursor [validated] - human
N.Alternate names: coagulation factor I; fibrinogen gamma-55 chain
C.Species: Homo sapiens (man)
C.Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text-change 08-Dec-2000
C.Accession: A90494; A92448; A90453; A28203; B28203; I37390; A03126
R.Rikun, M.W.; Chung, D.W.; Davie, E.W.
Biochemistry 24, 2077-2086, 1985
A.Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.
A.Reference number: A90494; MUID:85252774; PMID:2990550
A.Accession: A90494
A.Molecule type: DNA
A.Residues: 1-113,'T','I',115-453 <RIX>
A.Cross-references: GB:M10014; GB:J00134; GB:J00135; GB:X00066; NID:g182438; PIDN:AAB59595
R.Forname Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.
J. Biol. Chem. 259, 12826-12830, 1984
A.Title: Structure of the human gamma-B chain mRNA. Alternate mRNA splicing near the
A.Reference number: A92448; MUID:85030379; PMID:6092346
A.Accession: A92448
A.Molecule type: DNA
A.Residues: 286-453 <FOR>
R.Wolfenstein-Nodel, C.; Mosesson, M.W.
Biochemistry 20, 6146-6149, 1981
A.Title: Carboxy-terminal amino acid sequence of a human fibrinogen gamma-chain variant
A.Reference number: A90453; MUID:82068993; PMID:7306501
A.Accession: A90453
A.Molecule type: protein
A.Residues: 411-434,'Y','I',436-440,'Z','442','Z','444','B','446-447','R','449','ZBB','453 <WOL>
R.Francis, C.W.; Mueller, E.; Henschel, A.; Simpson, P.J.; Warder, V.J.
Proc. Natl. Acad. Sci. U.S.A. 85, 3358-3362, 1988
A.Title: Carboxyl-terminal amino acid sequences of two variant forms of the gamma-chain
A.Reference number: A94194; MUID:88217900; PMID:3368448
A.Accession: A28203
A.Molecule type: protein
A.Residues: 433-449 <FRA>
A.Accession: B28203
A.Molecule type: protein
A.Residues: 433-453 <FR2>
R.Marchetti, L.; Zanelli, T.; Malcovati, M.; Tenchini, M.L.
DNA Seq. 1, 419-422, 1991
A.Title: Polymorphism of the human gamma chain fibrinogen gene.
A.Reference number: I37390; MUID:92119334; PMID:1685103
A.Accession: I37390
A.Status: translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Residues: 75-286 <RES>
A.Cross-references: EMBL:X51473; NID:g31410; PIDN:CA35837.1, PID:g930064
C.Comment: The two forms of gamma chain, A (see PIR:FCHUG) and B, arise by alternate splicing, which makes this chain different from the gamma-B chain at positions 434-437 and 438-440.
C.Genetics: The gamma-B chain is present in about 10% of the fibrinogen molecules in plasma.
A.Gene: GDB:FGG
A.Cross-references: GDB:I19132; OMIM:134850
A.Map position: 4q28-4q28
A.Introns: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1
C.Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FCHUG) and beta chains are contained in the core. Two three-chain coiled coils emerge from this core and cross-link from the distal domain nodes.
C.Function:
A.Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into polymers called fibrin.
A.Pathway: blood coagulation
C.Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C.Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprotein; hemostasis
E:1-26/DNA: signal sequence #status predicted <SIG>
E:27-453/Product: fibrinogen gamma-B chain #status experimental <MPR>
E:176-415/DNA: fibrinogen beta/gamma homology <HBG>

```

E_741-355/Domain: calcium binding [status predicted <CAB>  

F_400-422/Region: polymerization site, binding to the amino end of the alpha chain of  

F_34/Dissulfide bonds: Interchain (to gamma-33) #status predicted  

F_35/Dissulfide bonds: Interchain (to gamma-33) #status predicted  

F_45/Dissulfide bonds: Interchain (to beta-110) #status predicted  

F_49/Dissulfide bonds: Interchain (to alpha-64) #status predicted  

F_78/Binding site: carbohydrate (Asn) (covalent) #status predicted  

F_161/Dissulfide bonds: Interchain (to beta-227) #status predicted  

F_165/Dissulfide bonds: Interchain (to alpha-180) #status predicted  

F_179-208,352-365/Dissulfide bonds: #status predicted  

F_424/Cross-link: Isopeptide (Gln) (Interchain to Lys-432 N6-amino) #status predicted  

F_432/Cross-link: Isopeptide (Lys) (Interchain to Gln-424) #status predicted
```

```

Query Match          17.7%; Score 371.5; DB 1; Length 453;
Best Local Similarity 31.9%; Pred. No. 1,8e-21;
Matches 105; Conservative 42; Mismatches 129; Indels 53; Gaps 11;
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QY      85 NSIVSTNSTRKLLRNMDQ-----QASLDYSNQVNELMNRVLLLTTEVFRKDLPF 138
       |||:::|||||:::|||:::|||||:::|||||:::|||||:::|||||:::
Db     103 NMIDAAVLTKSRMLEEMIKMEKSEALITHDSSIRYLIOEIYNSNNQKIVLNKEKV--AQLEAQ 160

QY     139 PRRP-----YOSH---GLDCTDIKDTIGSVTTPSGSLYIIHEGSSYPFEVNCDDMYRGG 191
       |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db     161 COEPCKDVYQHIDITGKKCD-----IANKGAKQSLEYIKPLKANQOFLVYCEIDSGNG 216

QY     192 WTVIQRKIDGIHFQRLWCDYLDGFGDL----LGEFWGLKIFYVQNKTSPMLVVAL 247
       |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db     217 WTVFQKRILDGSVFDEKKNVIQREGECHLSPTGTTFEVGNKHILHISQSAIPRALVEL 276

QY     248 ESEDOTLVASTADNWLEDETREFFMHLGRYS-GNAGDAFEGLKRED-----NONAM 298
       |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db     277 EDWNRTSTADYAMKRVPEADKYRLTYAPAGGACGAFPGFDGPDSKPFTHSHGM 336

QY     299 PSTSDVDNDGCRPACTLVNGOSVKCSHLHNKTMGFWEFCGLANLIGHHSGL----- 353
       |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db     337 QESTDNNDNDRFEGCAIQDGS-----GWNNKCHAGHLNGVYYTGQFSKRAST 385

QY     354 ---LATGIQWGTTWKNNSPVRIKVSMTKI 379
       |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db     386 PNGYDNGIIMATW--KTRNYSMKTKTKTI 412
```

```

RESULT 9
A38463
fibrinogen beta chain - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 13-Aug-1999
C:Accession: A38463
R:Weisbach, L.; Oddoux, C.; Procyk, R.; Grieninger, G.
Biochemistry 30, 3290-3294, 1991
A>Title: The beta chain of chicken fibrinogen contains an atypical thrombin cleavage
A:Reference number: A38463; MUID:91182745; PMID:2009246
A:Accession: A38463
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-463 <WEB>
A:Cross-references: MS:B58514; NID:g211779; PIDN:AAA48770.1; PID:g211780
F_73-202/Domain: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen dlsu
F_212-460/Domain: fibrinogen beta/gamma homology <FBG>
```

```

Query Match          17.7%; Score 371.5; DB 2; Length 463;
Best Local Similarity 27.7%; Pred. No. 1,8e-21;
Matches 112; Conservative 57; Mismatches 136; Indels 99; Gaps 17;
```

```

QY      61 CEESODVTKTRTREKHE-MCRNLONSIVSY--TRSTKILLRMMD----- 103
       |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db     80 CPYGCGLDTTLTKQEKTYKVPVLRDKRDVAKFSDSTSTMQYVMMDINKLVTKQGRKDN 139

QY     104 -----EQQASLDYSNQVNELMNRVLLLTTEVFRKDLPFPRPVYGS----- 145
       |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db    140 DILSEVTYEMELRYNIKDWLDNNIPSSLAVLRPAVIDSL-HKRTQKLLENALATQTIDYCR 198
```

```
OY 146 -----HGDCITDKITIGSVTTPSGLYIIHPEGSSYPFEVMDMDYRGGGT 193
DB 199 SPCVASCNIPVYSGRECEIYRKGGT-----SEMYIIQDPPTTPRYVYCDMETDNGGWT 254
OY 194 VIQKRIDGIIDPRLMCDYLDGFG-----DLGEFWLGLKKIRIYVQKNTSFM 242
DB 255 LIQNRQDGSVNGRADEYKRGFGNIAKSGKKYCDTPPEYVWGNDKISOLTKIGPTK-- 312
OY 243 LVVALESED---DTLAVASYDNFWELEDETRFEMHLGRYSGNAGDAF---RGLAKREDN- 294
DB 313 --VLIEMEDWNGDKYS-ALYGGFTIHNECNKYQLSVNKGNGNMLMBEASQLDYGENRT 369
OY 295 ---QNAAPSTSDVDNDGCRPACLVNGQSVKCSHLHNKGTFWNECGLANLNGIHFFSG 351
DB 370 WTIHNGMYSTYDRODNG-----WLTTPDKKQCK--EDGGGWVYNRCHAAHPNGRYWGG 423
OY 352 KL-----LATGIQWGTWTKNNSPVKIKSVSMKIRRMVNPYE 387
DB 424 TYSMDMAKHGTDGIVMNMN--KGSWYSMKKSMKIK----PYE 461
```

RESULT 10

```
A25052
fibrinogen beta chain - sea lamprey (fragments)
M:Contains: fibrinopeptide B
C:Species: Petromyzon marinus (sea lamprey)
C>Date: 25-Oct-1987 #sequence_revision 19-Feb-1999 #text_change 13-Aug-1999
C:Accession: A25052; A03124; B03124
R:Bohonus, V.L.; Doollittle, R.F.; Pontes, M.; Strong, D.D.
Biochemistry 25, 6512-6516, 1986
A>Title: Complementary DNA sequence of lamprey fibrinogen beta chain.
A:Reference number: A25052; MUID:87076582; PMID:3790537
A:Accession: A25052
A:Molecule type: mRNA
A:Residues: 39-479 <BO>
A:Cross-references: GB:M14773; NID:9213191; PIDN:AAA9261.1; PID:9213192
R:Cottrell, B.A.; Doollittle, R.F.
Biochim. Biophys. Acta 453, 426-438, 1976
A>Title: Amino acid sequences of lamprey fibrinopeptides A and B and characterization of
A:Reference number: A03120; MUID:77065679; PMID:99898
A:Accession: A03124
A:Molecule type: protein
A:Residues: 1-36 <CO1>
A:Accession: B03124
A:Molecule type: protein
A:Residues: 37-42 <CO2>
C:Superfamily: fibrinogen beta chain: fibrinogen beta/gamma homology; fibrinogen disulfide
C:Keywords: blood coagulation; glycoprotein; sulfoprotein
F:1-36/Product: fibrinopeptide B #status experimental <FPB>
F:37-479/Product: fibrin beta chain #status experimental <MAT>
F:90-219/Domain: fibrinogen disulfide ring homology <FDR>
F:229-477/Domain: fibrinogen beta/gamma homology <FBG>
F:13/Binding site: sulfate (Tyr) (covalent) #status experimental
F:27/Binding site: carbohydrate (Asn) (covalent) #status experimental
```

```
Query Match 17.6%; Score 370; DB 2; Length 479;
Best Local Similarity 28.9%; Pred. No. 2.5e-21;
Matches 108; Conservative 63; Mismatches 137; Indels 66; Gaps 17;
```

```
OY 45 NAKDEKSNIDYCKEDCE-----ESCDVTKIRIREEHFHFCRNQNSIVSYTRS 93
DB 130 NSFDRNASDSNTLKNVQTLRRRLNSRSSSTHVAQKEIENRYEKIR-IESTVAGSLRS 188
OY 94 TKLLNNMDEQOASLDYLSNQVNLNRRLLLTTEVFRKQDLPFPHRPVQSHGLDCTDI 153
DB 189 MKSVLEHLAKQRMKEAIKTQ-KELCSAPCTVNCRY-----PVS-GMHCEDI 235
OY 154 KDTIGSVTKPSGLYIIHPEGSSYPFEVMDMDYRGGGTWTVQKRIDGIIDPRLMCDYL 213
DB 236 YRNGGRITSEA---YYIQDPLFSEPYKVCDDMESHGSGWTVVQNRVDSGSNFARDWNTYK 291
OY 214 DGGNDL-----GEFWLGLKKIRIYVQKNTSFWLTVALSDEDTLAVASYDNF 262
```

```
DB 292 AEEGNIAFNGKSGICNIPGEYWLGTIVHQLTKQ-HTQOVLFDMSDEGSSV-YAQYASF 349
OY 263 WLDETRFEFMHLGRYSGNAGDA-FRLGK--IDNQ-----NAMPSTSDVDNDGCRPAC 314
DB 350 RPENEAGYRLWVEDYSGNAGNMLBEGATOLMDGNKRTMTIHNGMGSSTPDRDNNP-- 407
OY 315 LVNGQSVKCSHLHNKGTFWNECGLANLNGIHFFSG--KLLA-----TGQWGTWTKN 366
DB 408 ---GDPTKHCSR-EDAGGWVYNRCHAAHPNGRYWGGIYTKEDQADYGTDDGVVMMN--K 461
OY 367 NSPVKIKSVSMKIR 380
DB 462 GSWYSMRQAMKLR 475
```

RESULT 11

```
S05313
fibrinogen gamma-B chain precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Aug-1999
C:Accession: S05313
R:Brown, W.M.; Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R.
Nucleic Acids Res. 17, 6397, 1989
A>Title: Nucleotide and deduced amino acid sequence of a gamma subunit of bovine fibr
A:Reference number: S05313; MUID:89366676; PMID:2771651
A:Accession: S05313
A:Molecule type: mRNA
A:Residues: 1-444 <BO>
A:Cross-references: EMBL:X15556; NID:9349; PIDN:CA33562.1; PID:9350
A>Note: The authors translated the codon AAT for residue 105 as Ala and ATT for resid
C:Superfamily: fibrinogen gamma chain: fibrinogen beta/gamma homology
F:1-24/Domain: signal sequence #status predicted <SIS>
F:25-444/Product: fibrinogen gamma-B chain #status predicted <MAT>
F:174-414/Domain: fibrinogen beta/gamma homology <FBG>
```

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Query Match 17.3%; Score 365; DB 2; Length 444;
Best Local Similarity 30.2%; Pred. No. 5.7e-21;
Matches 100; Conservative 51; Mismatches 124; Indels 56; Gaps 12;
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```
OY 85 NSIVSYTRSKTKLLRNMN-----DEQOASLDYLSNQVNLNRRVLLLTTEVFRKQDLP 138
DB 101 NNIESATKNSKSMEEITKYTELTISTHETIRLQEYVNSNOKIYNLRDKV--OLEAN 158
OY 139 PRRPVOS-----HGDCITDKITIGSVTTPSGLYIIHPEGSSYPFEVMDMDYRGGG 191
DB 159 CGPRCQDVTYVHIVYGDGDD-----VANKGAKESGLTFIRPL-KAQOFLYCCIDDSGNG 213
OY 192 WYIYQKRIDGIIDPRLMCDYLDGFGDL-----GEFWLGLKKIRIYVQKNTSFWLYV 245
DB 214 WYFQKRIDGSLDFKKNWIOYKKEFGHLISPTGTGNTFEFWGNEKIHILISYSSIPYVLR 273
OY 246 ALSESDTLAVASYDNFWELEDETRFEMHLGRY-SGNAFAGLKKED-----NON 296
DB 274 QLEDWNGRTSTADYASFKVYGVENDKRYLYAVYITGGAGAFGVDGDDSSDKFTTSHN 333
OY 297 AMPFSTSDVDNDGCRPACLVNGQSVKCSHLHNKGTFWNECGLANLNGIHFFSGKLLAT 356
DB 334 GMPFSTWSDNDKYYDGC--AEQY-----GIGMMNKKAGHLNGVYGGCTYSKRT 382
OY 357 -----GIQWGTWTKNNSPVKIKSVSMKI 379
DB 383 STENGVDNGIIMATW--KSRWYSMKKTKYTKI 411
```

RESULT 12

```
FEGLMS
fibrinogen gamma chain precursor - sea lamprey
C:Species: Petromyzon marinus (sea lamprey)
C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 20-Oct-2000
C:Accession: A03129
R:Strong, D.D.; Moore, M.; Cottrell, B.A.; Bohonus, V.L.; Pontes, M.; Evans, B.; Rile
Biochemistry 24, 92-101, 1985
A>Title: Lamprey fibrinogen gamma chain: cloning, cDNA sequencing, and general charac
```



```

QY 313 ACIACGSCGSCSH-LNKKTGMWMECEGLANLNGIHH-FSGKLLAAGIOWGTWTKNNSPV 370
Db 219 -----VYSINASHSSISVGRGAMWTKSCLLSLNNGQYIDYSG---APSTIYSYLPGRND-- 268
QY 371 KIKSVSMKIR 380
Db 269 QIPFAEMKIR 278

```

RESULT 15
A39832

scabrous locus (scs) protein precursor - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 01-Dec-2000
C:Accession: A39832, S58998
R:Baker, N.E.; Mlodzik, M.; Rubin, G.M.
Science 250, 1370-1377, 1990
A:Title: Spacing differentiation in the developing *Drosophila* eye: a fibrinogen-related
A:Reference number: A39832; MUID:91075223; PMID:2175046
A:Accession: A39832
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-774 <BAK>
A:Cross-references: GB:M60065; GB:M37703; NID:g158401; PID:g158402
R:Hu, X.; Lee, E.C.; Baker, N.E.
Genetics 141, 607-617, 1995
A:Title: Molecular analysis of scabrous mutant alleles from *Drosophila melanogaster* indi
A:Reference number: S58998; MUID:96109607; PMID:8647337
A:Accession: S58998
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-18, 'T', 20-774 <HUX>
C:Genetics:
A:Gene: FlyBase:scs
A:Cross-references: FlyBase:FBgn0003326
C:Superfamily: fibrinogen beta/gamma homology
F:514-711/Domain: fibrinogen beta/gamma homology <FBG>

Search completed: December 16, 2002, 17:36:20

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5

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 16, 2002, 17:27:23 ; Search time 9.2381 Seconds

(Without alignments)
1742.006 Million cell updates/sec

Title: US-09-596-196-4

Perfect score: 2104
Sequence: 1 MMSPSQASLLFLNVCIFG.....PVKIKSVSMKIRRMNPFYK 388

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	413.5	19.7	439	1	Q14314 homo sapien
2	405.5	19.3	432	1	P12804 mus musculu
3	400.5	19.0	481	1	Q18920 bos taurus
4	400.5	19.0	493	1	Q91045 mus musculu
5	398	18.9	493	1	Q91045 mus musculu
6	395.5	18.8	468	1	P02676 bos taurus
7	395	18.8	468	1	P02676 bos taurus
8	391	18.6	498	1	Q15389 homo sapien
9	381.5	18.1	496	1	Q08538 mus musculu
10	375.5	17.8	491	1	O15123 homo sapien
11	375.5	17.8	491	1	P02675 homo sapien
12	375	17.8	375	1	O35608 mus musculu
13	374.5	17.8	496	1	P14480 ratu
14	373.5	17.8	479	1	P14480 ratu
15	371.5	17.7	453	1	P02679 homo sapien
16	371.5	17.7	463	1	P02020 gallu
17	370	17.6	477	1	P02678 petromy
18	365	17.3	444	1	P12769 bos taur
19	363	17.3	432	1	P04115 petromy
20	360	17.1	509	1	Q91045 mus musculu
21	358	17.0	503	1	Q91045 mus musculu
22	353	16.8	438	1	P17634 xenopus lae
23	351	16.7	319	1	P57756 ratu
24	350.5	16.7	282	1	P19477 parastichop
25	348.5	16.6	774	1	P15570 drosophila
26	337.5	16.0	866	1	P02671 homo sapien
27	335.5	15.9	741	1	P14448 gallu
28	332	15.8	306	1	O70497 mus musculu
29	329.5	15.7	641	1	P33573 petromy
30	329	15.6	334	1	O70165 mus musculu
31	327.5	15.6	445	1	P02680 ratu
32	321.5	15.3	313	1	Q15485 homo sapien
33	321	15.3	255	1	P55083 homo sapien

34	313.5	14.9	782	1	F1BA_RAT	P06399 ratu
35	310.5	14.8	1808	1	TENA_CHICK	P10039 gallu
36	308.5	14.7	326	1	FCN1_HUMAN	O00602 homo sapien
37	305.5	14.5	335	1	FCN1_RAT	O9158 ratu
38	302.5	14.4	4289	1	TENX_HUMAN	P22105 homo sapien
39	291	13.8	299	1	FCN3_HUMAN	O75636 homo sapien
40	282.5	13.4	1746	1	TENA_PIG	Q29116 sus scrofa
41	271	12.9	2201	1	TENA_HUMAN	P24821 homo sapien
42	197	9.4	137	1	AGP2_RAT	O35462 ratu
43	109	5.2	129	1	MEP4_BOVIN	P55918 bos taurus
44	99.5	4.7	586	1	PMEL_ARATH	O43867 arabidopsis
45	99	4.7	599	1	YAQB_SCHPO	Q10110 schizosach

ALIGNMENTS

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RESULT 1
FGL2_HUMAN          STANDARD:      PRT:  439 AA.
ID                  Q14314;
AC                  16-OCT-2001 (Rel. 40, Created)
DT                  16-OCT-2001 (Rel. 40, Last sequence update)
DE                  15-JUN-2002 (Rel. 41, Last annotation update)
DE                  Fibrinogen-like protein 2 (p7149).
GN                  FGL2.
OS                  Homo sapiens (Human).
OC                  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC                  Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX                  NCBI_TaxID=9606;
RN                  [1]
RP                  SEQUENCE FROM N.A.
RC                  TISSUE=Small intestine;
RX                  MEDLINE=95369700; PubMed=7642106;
RA                  Ruegg C., Pyela R.;
RT                  "Sequence of a human transcript expressed in T-lymphocytes and
RL                  encoding a fibrinogen-like protein.";
RL                  Gene 160:257-262(1995).
RN                  [2]
RP                  SEQUENCE FROM N.A.
RA                  Yuvaraj S., Liu M., Marsden P., Levy G.;
RT                  "Cloning and characterization of Hg12: the human counterpart to the
RL                  mouse gene Fg12.";
RN                  [3]
RP                  Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
RA                  Rieder M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA                  Poel C.L., Ozuna M., Yi Q., Nickerson D.A.;
RN                  Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
RX                  MEDLINE=98309432; PubMed=9647217;
RA                  Maraziti S., Blum S., Hartmann R., Gundersen D., Schreyer M.,
RA                  Argaves S., von Fliedner V., Pyela R., Ruegg C.;
RT                  "Characterization of human fibrinogen-like protein
RL                  secreted by T lymphocytes.";
RL                  J. Immunol. 161:138-147(1998).
CC                  -1- FUNCTION: MAY PLAY A ROLE IN PHYSIOLOGIC LYMPHOCYTE FUNCTIONS AT
CC                  MUCOSAL SITES.
CC                  -1- SUBUNIT: HOMOTETRAMER; DISULFIDE-LINKED.
CC                  -1- SUBCELLULAR LOCATION: Secreted.
CC                  -1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC
CC                  T-CELLS.
CC                  -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC                  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC                  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC                  the European Bioinformatics Institute. There are no restrictions on its
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CC                  or send an email to license@isb-sib.ch).

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DR EMBL: Z36531: CAA85298.1: -
DR EMBL: AF104015: AAD10825.1: -
DR EMBL: AF104014: AAD10825.1: JOINED.
DR EMBL: AF468959: AAL68855.1: -
DR HSSP: P02671: 1FZD.
DR Genew: HGNC:3696: FGL2.
DR MIM: 605351: -
DR InterPro: IPR002181: Fibrinogen_C.
DR Pfam: PF00147: Fibrinogen_C; 1.
DR SMART: SM00186: FBG; 1.
DR PROSITE: PS00514: FIBRIN-AG-C-DOMAIN; 1.
KW T-cell; Glycoprotein; Signal; Polymorphism.
FT SIGNAL 1 23
FT CHAIN 24 439
FT DOMAIN 210 435
FT DISULFID 213 242
FT DISULFID 371 384
FT CARBOHYD 25 25
FT CARBOHYD 179 179
FT CARBOHYD 235 235
FT CARBOHYD 263 263
FT CARBOHYD 336 336
FT VARIANT 53 53
/FTID=VAR_013066.
SEQUENCE 439 AA: 50228 MW: DP34656288EA9E68 CRC64:

Query Match 19.7%; Score 413.5; DB 1; Length 439;
Best Local Similarity 30.2%; Pred. No. 2.1e-25;
Matches 119; Conservative 61; Mismatches 147; Indels 67; Gaps 15;

OY 34 SSVVNIIVEGCSNAKDESKNDVCKEDC-----ESCQVTKK 70
DB 73 SIEEEVEKQVQLKTIWLSLKSC-QDCKLQADNGDPGRNGILLPSTGAPEVEGDNRR 131
OY 71 ITRREEHFCMRLQNS---IVSYRSTKTLRNM-----MDEQASLDYLSNQNVEIM 120
DB 132 ELESEVNRKLSSELKNAKEINVLHGRLKLNLYNMNNIENVDSKAVANLTFVNSLDGNC 191
OY 121 NRVLLITTEVFRKQLDPPRHVQSHGL-DCTDIKDTIGSVTKPPSGLYIHPGSSYR 178
DB 192 SKC-----PSQEOIOSRPVQ-HLYKDCSDYV---AIGKRSSEYRVTPDPKNS 237
OY 179 FVVMCDMDYRGSGMTVIQKRIIDIFORLMCDYLDGFGDILGFMLGKIFLYINOKN 238
DB 238 FEYVCDMEIAGGWTYVLRKLDGSGTNFTTWDYKAGFENLRERMLGDKIHLTL--KS 295
OY 239 TSFMLYVALESDPTLAAVADNFMLEDETRFKMHLGRYSNAGDAFGLKKEQNQNM 298
DB 296 KEMILRIIDLEDENGVELVALYDQFYVANEFLRYLHVGNVGTAGDALR-FKHYNHDLK 354
OY 299 PSTSDVDNDGCRPACLVNGOSVSKSHLHNTGWMFNECGLANLNG-IHFSGLLATG 357
DB 355 FETTDKNDKNDRYPSG-----NCG-LYSSGWMFDACLASANLNGKYHOKYRGVRNG 404
OY 358 IOWGTW--TKNSPYKISVSMKIRRYNP-YFK 388
DB 405 IFWGTWPGVSEAHPGYKSSFEKAKMIRPKHFK 438

RESULT 2
FGL2_MOUSE
ID FGL2_MOUSE STANDARD; PRT; 432 AA.
AC P12804:
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibrinoleukin precursor (fibrinogen-like protein 2) (Prothrombinase)
DE (Cytotoxic T-lymphocyte specific protein).
GN FGL2 OR FIBLP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cytotoxic T-cell;
RA MEDLINE=87175527; PubMed=3550794;
RX Koyama T., Hall L.R., Hasegawa S., Salto H.
RT "Structure of a cytotoxic T-lymphocyte-specific gene shows a strong
RT proc. Natl. Acad. Sci. U.S.A. 84:1609-1613(1987).
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=BAH/CJ; TISSUE=peritoneal macrophage;
RX MEDLINE=95333285; PubMed=7609073;
RA Parr R.L., Fung L., Reneker J., Myers-Mason N., Leibowitz J.L.,
RA Levy G.;
RT "Association of mouse fibrinogen-like protein with murine hepatitis
RT virus-induced prothrombinase activity.";
RL J. Virol. 69:5033-5038(1995).
CC -1- FUNCTION: CONVERTS PROTHROMBIN TO THROMBIN.
CC -1- SUBUNIT: HOMOTETRAMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC
CC T-CELLS.
CC -1- INDUCTION: IN MACROPHAGES, DURING INFECTION BY MOUSE HEPATITIS
CC VIRUS STRAIN 3 (MHV-3) FIBRINOGEN C-TERMINAL DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: M16238: AAA37624.1: -
DR EMBL: M15761: AAA37624.1: JOINED.
DR EMBL: S78773: AAB34823.1: -
DR PIR: A27447; A27447.
DR HSSP: P02671: 1FZD.
DR MGD: MGI:103266; Fgl2.
DR InterPro: IPR002181: Fibrinogen_C.
DR Pfam: SM00147: fibrinogen_C; 1.
DR SMART: SM00186: FBG; 1.
DR PROSITE: PS00514: FIBRIN-AG-C-DOMAIN; 1.
KW T-cell; Cytolysis; Signal.
FT SIGNAL 1 19
FT CHAIN 20 432
FT DOMAIN 203 428
FT DISULFID 206 235
FT DISULFID 364 377
FT CARBOHYD 24 24
FT CARBOHYD 172 172
FT CARBOHYD 228 228
FT CARBOHYD 256 256
FT CARBOHYD 329 329
FT CONFLICT 332 332
SQ SEQUENCE 432 AA: 48951 MW: 28297690CBA4782 CRC64;
Query Match 19.3%; Score 405.5; DB 1; Length 432;
Best Local Similarity 35.4%; Pred. No. 8.9e-25;
Matches 110; Conservative 43; Mismatches 115; Indels 43; Gaps 13;

QY 258 SYDNFLEDETRFFKMLHGRYSGNAGDAFRGLKEDNQNAMPSTSDVNDGCRPACTVN 317
 DB 308 LVDQFVYANEFELKRYLHIGYNGTADALR-FSRHYNHDRFFFTTPDRDNDPSPSG---- 362
 QY 318 GQSVKSGSHLHNTGMWNEBCGLANLNG-IHHSFGKLATGIOMGWTKNN--SPVAKRS 374
 DB 363 -----NCG-LIYSGWFWDSCLSANLNGKYHOKRGVNRITGWTGPIQAOAGGYSK 416
 QY 375 VSMKIRMYNP 385
 DB 417 SFGQAKMTRP 427

RESULT 3
 ID AGPI_BOVIN STANDARD; PRT; 481 AA.
 AC 018930:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Angiotensin-1 precursor (ANG-1) (Fragment).
 GN ANGPT1 or ANG1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 ON NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Ovary;
 RX MEDLINE=99054348; PubMed=9840613;
 RA Goede V., Schmidt T., Kimmina S., Kozian D., Augustin H.G.;
 RT "Analysis of blood vessel maturation processes during cyclic ovarian
 RT angiogenesis.";
 RL Lab. Invest. 78:1385-1394(1998).
 RN [2]
 RP SEQUENCE OF 91-200 FROM N.A.
 RC TISSUE-Liver;
 RX MEDLINE=98451564; PubMed=9776732;
 RA Mandiote S.J., Pepper M.S.;
 RT "Regulation of angiotensin-2 mRNA levels in bovine microvascular
 RT endothelial cells by cytokines and hypoxia.";
 RL Circ. Res. 83:852-859(1998).
 CC -1- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS
 CC TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
 CC PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
 CC CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
 CC ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
 CC VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
 CC HEART EARLY DEVELOPMENT (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DEVELOPMENTAL STAGE: FOUND TO BE EXPRESSED THROUGHOUT THE OVARIAN
 CC CYCLE.
 CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AF093573; AAC61872.1; -;
 CC EMBL: AF032923; AAC78245.1; -;
 CC HSSP: P02671; IFZD.
 CC InterPro: IPR002181; Fibrinogen_C.
 CC Pfam: PF00147; Fibrinogen_C; 1.
 CC SMART: SM00186; FBG; 1.
 CC PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
 KM Glycoprotein; Coiled coil; Signal.
 FT SIGNAL 1 15 POTENTIAL.

FT CHAIN 16 >481 ANGIOPOIETIN-1.
 FT DOMAIN 153 261 COILED COIL (POTENTIAL).
 FT FIBRINOGEN C-TERMINAL.
 FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 243 243 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 481 481
 SQ SEQUENCE 481 AA; 55556 MW; 8EEC9ED84FC2BB50 CRC64;

Query Match 19.0%; Score 400.5; DB 1; Length 481;
 Best Local Similarity 27.9%; Pred. No. 2; Se-24;
 Matches 114; Conservative 60; Mismatches 116; Indels 119; Gaps 15;

QY 23 VQNCVHSTDSVYVNIIVEGNSNAKDESKSNDYCKEDCESGCKVTKITREEHFACRN 82
 DB 115 IQQNAVONHT-----ATMLEIGTSLST-----AQTRKLDVETQVLNQTSLREIQL 163
 QY 83 LQNSIVSY-----
 DB 164 LENSLSYKLEKQLQOQTNELIKHEKNSLLEHKIFEMEGKHKELDPTLKEKKNLQGLV 223
 QY 103 DEQASLDIYSNOVN-----ELM-----NRULLTTEVF-----RKQLDPP 139
 DB 224 TRQTYIIQLELEKOLNRRATTNNSVLOKQOLEMDTVHMLVNLCKREYLLKGGRKEEPF- 282
 QY 140 HRPVQSHGLDCTDIDKIDTIGSVTKTPSGIYIIHPGSSYPPFVMDMDYRGSGWTVIOKRI 199
 DB 283 -----RQCADY-----QAGFNKSGIYIYIYINMEPEKPVFCMDMLNGGWTIOHRE 330
 QY 200 DGIIDFORLNCMDYLDGFGLLGEFLLGLKIFYIVNOKNTSFMLYVALSEDDTLAYASY 259
 DB 331 DGSIDPFGRMKVEYKMGFNGSGEYWLGNFIFATTSR--QYLRILDLMEGRRAISQY 388
 QY 260 DNFWEDETRFFKMLHGRYSGNAGDAFRGLKEDN--QNAMPSTSDVNDGCRPAC--L 315
 DB 389 DRFHIGNEKQNYRLYLGHGTAG-----KQSLIHGADFSTKADADNMCCKCALM 441
 QY 316 VNGSVKSGSHLHNTGMWNEBCGLANLNGIHHS-----CKLATGIOW 360
 DB 442 LTG-----GWFMDACGSPNLNGMFTYAGNHGKL--NGIKW 475

RESULT 4
 ID ANL2_MOUSE STANDARD; PRT; 493 AA.
 AC Q9R045:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Angiotensin-related protein 2 precursor (Angiotensin-like 2).
 GN ANGPTL2 OR ARP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Heart;
 RX MEDLINE=99403103; PubMed=10473614;
 RA Kim I., Moon S.-O., Koh K.N., Kim H., Uhm C.-S., Kwak H.J., Kim N.-G.,
 RA Koh G.-Y.;
 RT "Molecular cloning, expression, and characterization of angiotensin-
 RT related protein, angiotensin-related protein induces endothelial cell
 RT sprouting.";
 RL J. Biol. Chem. 274:26523-26528(1999).
 CC -1- FUNCTION: INDUCES SPROUTING IN ENDOTHELIAL CELLS THROUGH AN
 CC AUTOCRINE AND PARACRINE ACTION (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEART, TONGUE, LUNG AND
 CC SKELETAL MUSCLE. ALSO FOUND IN LOWER LEVELS IN KIDNEY, EPIDIDYMUS
 CC AND TESTIS.

CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
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CC
DR EMBL; AF125176; AAD5358.1; -
DR HSSP; P02671; 1PZD.
DR MGP; MGI:1347002; Angp12.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN-AG-C-DOMAIN; 1.
KW Signal; Colled coil; Glycoprotein.
FT CHAIN 1 19 POTENTIAL.
FT SIGNAL 1 19 ANGIOPROTEIN-RELATED PROTEIN 2.
FT DOMAIN 77 115 COILED COIL (POTENTIAL).
FT DOMAIN 152 202 COILED COIL (POTENTIAL).
FT DOMAIN 438 450 FIBRINOGEN C-TERMINAL.
FT CARBOHYD 164 164 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNC. . .) (POTENTIAL).
SQ SEQUENCE 493 AA; 57118 MW; 22855ABE0746BF2 CRC64;

Query Match 19.0%; Score 400.5; DB 1; Length 493;
Best Local Similarity 26.7%; Pred. No. 2.6e-24;
Matches 107; Conservative 66; Mismatches 107; Indels 121; Gaps 15;

OY 68 KKIRREHFRCRLQNSIVSTSTKLLRNMDQASDLYLSNOVNEMLNRVLLT 127
DB 119 EKLRLKES---RNNNSRV---TOLYQLLHEIIRKRNAL---ELSOLENRILNQT 166
OY 128 TEVFR---KOLD-----GLDCTDIDTIGSVTKTPSG-----PEPIRP----- 142
DB 167 ADMQLASKYKDLKHFQHLAHLAINOSFVIAOLEHCORVAPARMPPPRAAPRVYQ 226
OY 143 -----VQSH-----GLDCTDIDTIGSVTKTPSG----- 166
DB 227 PTYNRRIINQISTNEIOSQNLKVLPPSLPTPALTSIPSSYDCKSGSPRDCIQALEDDH 286
OY 167 ---YIIHPGSSYPEFYWCMDYRGGWVYIOKRIGIIDFORIMCVDLGGFDLLGE 222
DB 287 STSSYLVKPEPTNRLMQVWCQDRHDPGGWTVIQRKLDSEVNEFRKWEYKQGFNIDGE 346
OY 223 FWLGLKRTFYIVNOKNTSEMLYVALESEDDTLAYASYDNFWLEDETRFFKMLGRYSNA 282
DB 347 YWLGLENYIWLNGCN--YKLLVTMEDMSGKRVAFVAFSFLPESEYKRLGLRGHNA 404
OY 283 GDAFGLKKEKNQNMAMPSTSDVNDGCRPACLVNGOSVKSCHLHNKTGMWNECCGAN 342
DB 405 GDSFTW-----HNGKQFTTLDHRD-----VYTG---NCAH-YQKGWVYNACAHN 447
OY 343 LINGIHFGSKLLA---TGIOGWTYTKNNSPVKIKSVSMKIR 380
DB 448 LMGVMTRGHYSRYQDGYVAEF--RGGSYSLLKRVMMIR 486

RESULT 5
ANL2_HUMAN
ID ANL2_HUMAN STANDARD; PRT; 493 AA.
AC Q9UKU9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiopoietin-related protein 2 precursor (Angiopoietin-like 2).
GN ANGPTL2 OR ARP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=99403103; PubMed=10473614;
RA Kim I., Moon S.-O., Koh K.N., Kim H., Uhm C.-S., Kwak H.J., Kim N.-G.,
RA Koh G.Y.;
RT "Molecular cloning, expression, and characterization of angiopoietin-
RT related protein, angiopoietin-related protein induces endothelial cell
RT sprouting";
RL J. Biol. Chem. 274:26523-26528(1999).
CC -1- FUNCTION: INDUCES SPROUTING IN ENDOTHELIAL CELLS THROUGH AN
CC AUTOCRINE AND PARACRINE ACTION.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEART, SMALL INTESTINE,
CC SPLEEN AND STOMACH. ALSO FOUND IN LOWER LEVELS IN COLON, OVARY,
CC ADRENAL GLAND, SKELETAL MUSCLE AND IN PROSTATE.
CC -1- PTM: N-GLYCOSYLATED.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC
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CC or send an email to license@sdb-sdb.ch).
CC
DR EMBL; AF125175; AAD5357.1; -
DR HSSP; P02671; 1PZD.
DR GeneW; HGNC:490; ANGPTL2.
DR MIM; 605001; -
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN-AG-C-DOMAIN; 1.
KW Signal; Colled coil; Glycoprotein.
FT CHAIN 1 22 POTENTIAL.
FT SIGNAL 1 22 ANGIOPROTEIN-RELATED PROTEIN 2.
FT DOMAIN 76 115 COILED COIL (POTENTIAL).
FT DOMAIN 152 206 COILED COIL (POTENTIAL).
FT DOMAIN 438 450 FIBRINOGEN C-TERMINAL.
FT CARBOHYD 164 164 N-LINKED (GLCNC. . .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNC. . .) (POTENTIAL).
SQ SEQUENCE 493 AA; 57104 MW; 0F2ADECE35D185CA CRC64;

Query Match 19.0%; Score 400; DB 1; Length 493;
Best Local Similarity 31.9%; Pred. No. 2.9e-24;
Matches 94; Conservative 50; Mismatches 93; Indels 58; Gaps 11;

OY 117 NELMRVLLTEVFRKQ---LDPFPIRPVQSHGLDCTDIKDTIGSVTKTPSG----- 166
DB 231 NRIINOI--STNEIOSDQMLKVLPPPLPMLPTLT-----SLPSSYDCKSGSPWRDC 278
OY 167 ---YIIHPGSSYPEFYWCMDYRGGWVYIOKRIGIIDFORIMCVDLGGFDLLGE 222
DB 279 LQALEDHGHTSSYLVKPEPTNRLMQVWCQDRHDPGGWTVIQRKLDSEVNEFRKWEYKQGFNIDGE 346
OY 215 GFGDLLGEFNLGLKRTFYIVNOKNTSEMLYVALESEDDTLAYASYDNFWLEDETRFFKML 274
DB 339 GFGNIDGEYWLGLENYIWLNGCN--YKLLVTMEDMSGKRVAFVAFSFLPESEYKRL 396
OY 275 LGRTSGNAGDAFGLKKEKNQNMAMPSTSDVNDGCRPACLVNGOSVKSCHLHNKTGMW 334
DB 397 LGRYHGNAGDSFTW-----HNGKQFTTLDHRD-----VYTG---NCAH-YQKGW 439
OY 335 FNECCGANLNGIHFGSKLLA---TGIOGWTYTKNNSPVKIKSVSMKIR 380
DB 440 YNACAHSNLNGVMTRGHYSRYQDGYVAEF--RGGSYSLLKRVMMIR 486

RESULT 6
FGL1_HUMAN
ID FGL1_HUMAN STANDARD; PRT; 312 AA.

AC 008830; 0960M6; 096KM6;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fibrinogen-like protein 1 precursor (Hepatocyte-derived fibrinogen-
 related protein 1) (HFRP-1) (Hepasocin) (HP-041).
 GN FGL1 OR HFRP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=93290661; PubMed=8390249;
 RA Yamamoto T., Gotoh M., Sasaki H., Terada M., Kitajima M.,
 Hirohashi S.;
 RT "Molecular cloning and initial characterization of a novel
 fibrinogen-related gene, HFRP-1.";
 RL Biochem. Biophys. Res. Commun. 193:681-687(1993).
 RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=2163035; PubMed=11470158;
 RA Hara H., Yoshimura H., Uchida S., Toyoda Y., Aoki M., Sakai Y.,
 Morimoto S., Shiohara K.;
 RT "Molecular cloning and functional expression analysis of a cDNA for
 human hepasocin, a liver-specific protein with hepatocyte mitogenic
 activity.";
 RL Biochim. Biophys. Acta 1520:45-53(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Has hepatocyte mitogenic activity.
 CC -1- SUBUNIT: Homodimer (Probable).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Liver-specific.
 CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D14446; BAA0336.1; -;
 DR EMBL: D67342; BAB70690.1; -;
 DR EMBL: BC007047; AAH07047.1; -;
 DR HSSP: P02671; 1FZD.
 DR GeneW: HGNC:3695; FGL1.
 DR MIM: 605776; -;
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C; 1.
 DR SMART: SM00186; FBG; 1.
 DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
 KM Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 312 FIBRINOGEN-LIKE PROTEIN 1.
 FT DOMAIN 78 305 FIBRINOGEN C-TERMINAL.
 FT DISULFID 26 26 INTERCHAIN (POTENTIAL).
 FT DISULFID 83 112 BY SIMILARITY.
 FT DISULFID 248 261 BY SIMILARITY.
 FT CONFLICT 15 15 I -> T (IN REF. 3).
 FT CONFLICT 69 69 N -> D (IN REF. 1).
 FT CONFLICT 72 72 I -> V (IN REF. 1).
 FT CONFLICT 105 105 P -> L (IN REF. 2).
 SO SEQUENCE 312 AA; 36391 MW; 26BC82124E660C2 CRC64;

Query Match 18.98; Score 398; DB 1; Length 312;

Best Local Similarity 34.38; Pred. No. 2.3e-24;
 Matches 111; Conservative 44; Mismatches 115; Indels 54; Gaps 12;
 QY 87 IVSYRSTKRLRMMDQASLDLYLSNOVLENNRVLITTEFRRO----- 134
 DB 4 VFSFILTVALT---KRETSALDECAQEQRLAQLVLETRKQOQVRIKOLLQENEV 60
 QY 135 --LDPFPRPVQSHG-----LDCTDIRDTIGSVYKTPSGYIIHPESGSYPFEVCMNDY 187
 DB 61 QFLDKGDNVYIDGSRKQYADGSEIFNDGKL-----SGFYKIRPLQSPAFSYCCMS- 115
 QY 188 RGGGTVYQKRIDGIDIPRLMCDYLDGFDLL--GEFWLGLKIFYINQKNTSPMLY 244
 DB 116 DGGGTVYQKRSDSENFNGMKDYENGFGFVQKHGEYVGNKNNHFLTQED--YTLK 173
 QY 245 VALESDDTLAVASDYDPFLEDEFKFMHIGRYSNAGAFRLKKEDNO-----NAMP 299
 DB 174 IDLADFEKNSRYAQYKFKYGDENFELNIGETSGAGSLAGNFPYQWMAHORMK 233
 QY 300 FSTSDVDNDCRPACLVNGSVKSCSHLHNKGMWMECGLANINGIHRSGLKLA--T 356
 DB 234 FSTWDRDHNDVEGCAEDDS-----GWMFNRCHSANLNGV-YSGPYTAKTDN 281
 QY 357 GIGMGTVTKNNSPVYKISVSKIR 380
 DB 282 GIWVYTW--HGWMYSLKSVYMKIR 303
 RESULT 7
 FIBB_BOVIN STANDARD; PRT; 468 AA.
 ID FIBB_BOVIN
 AC P02676;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
 GN FGB.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 ON NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE OF 1-4.
 RA Blomback B., Doolittle R.F.;
 RT "The sequence of amino acids at the N-terminal end of bovine
 fibrinopeptide B.";
 RL Acta Chem. Scand. 17:1816-1819(1963).
 RN [2]
 RP SEQUENCE OF 5-21.
 RA Sjoquist J., Blomback B., Wallen P.;
 RT "Amino acid sequence of bovine fibrinopeptides.";
 RL Ark. Kemi 16:425-436(1960).
 RN [3]
 RP SEQUENCE OF 22-53.
 RX MEDLINE=79164394; PubMed=434821;
 RA Martineelli R.A., Ingilis A.S., Rubira M.R., Hageman T.C.,
 RA Hurrell J.G.R., Leach S.J., Scheraga H.A.;
 RT "Amino acid sequences of portions of the alpha and beta chains of
 bovine fibrinogen.";
 RL Arch. Biochem. Biophys. 192:27-32(1979).
 RN [4]
 RP SEQUENCE OF 44-468 FROM N.A.
 RX MEDLINE=81199473; PubMed=626803;
 RA Chung D.W., Rixon M.W., McGillivray R.T.A., Davie E.W.;
 RT "Characterization of a cDNA clone coding for the beta chain of bovine
 fibrinogen.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:1466-1470(1981).
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C; 1.
DR SMART: SM00186; FBG; 1.
DR PROSITE: PS00514; FIBRIN-AG_C_DOMAIN; 1.
KW Glycoprotein; Coiled coil; Signal; Polymorphism.
FT SIGNAL 1 15
FT CHAIN 16 498
FT DOMAIN 81 119
FT DOMAIN 153 261
FT DOMAIN 284 498
FT CARBOHYD 92 92
FT CARBOHYD 122 122
FT CARBOHYD 154 154
FT CARBOHYD 243 243
FT CARBOHYD 295 295
FT VARIANT 269 269
FT FT MISSING (IN CELL LINE T98G; MAY BE DUE TO EXON SLIPPAGE).
FT FT /FTID-VAR-009940.
SQ SEQUENCE 498 AA; 57513 MM; 5D5FA63AEFBEB920 CRC64;
Query Match 18.8%; Score 395; DB 1; Length 498;
Best Local Similarity 27.0%; Pred. No. 7, 2e-24;
Matches 116; Conservative 66; Mismatches 126; Indels 122; Gaps 16;
QY 23 VQNCVHSHSTDSVYNIVEDGSKNADESKSNDYCKEDCEESCDYKTKITREKHFMCRN 82
DB 115 IQQNAVONHT---ATMLEIGTSLISQT-----AEQTRKLTVEYOVNLQTSRLLEIQL 163
QY 83 LQNSIVSY-----TRSTKILRLNMM 102
DB 164 LENSLSYKLEKOLLQOTNEILKTHEKNSLLEHKLLEMEGKHKEELDTLKEEKENLQGLV 223
QY 103 DEQASLDYLSNOYV-----ELM-----NRVLLLTVEF-----RKQLDPF 138
DB 224 TRQYIIQLELEKQKRNATNNNSVLQKQOELMDVYHNLVNCSTEGVLLKKGKREEKRF 283
QY 139 PRRPVQSHGLDCTDIKDTIGSVTKPSGLYTIHREGSSYPREVNCMDYRGSGWTYQKR 198
DB 284 -----RDCADVY-----QAGFNKSGIYIYINNMPEKPKVCNMDVNGCGWTYIOHR 330
QY 199 IDGIIDFQRLMCDYLDGFGDLGFEWLGKIKFIYVQKNKSFMLYVALBESDPTLAYAS 258
DB 331 EDGSLDFQRGKKEYKMGFGNPSGEYWLGNFIYATISOR--QYMLRIELMDWENRAYSQ 388
QY 259 YDNFWLEDETRFEKMLGKRYSGNAGDAFRGLKKEEDN--QNAAPRSTSDVDNDGCRPAC-- 314
DB 389 YDRHIGNENQNYRLYLKHTGTAG-----KQSSILHGADESTDADNDNCMCAL 441
QY 315 LVNGQSVKSCSHLHNTKGMWFNECGLANLNGIHHS-----GKLATGIGQMTWTKNNSPV 370
DB 442 MLC-----GWWFDACGPNLNGMFTYAGQNHGKL--NGIKWHYF--KGPSY 484
QY 371 KIKSVSMKIR 380
DB 485 SLKSTYIMIR 494
RESULT 9
AGPL_MOUSE STANDARD: PRT: 498 AA.
ID AGPL_MOUSE 008336;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiopoietin-1 precursor (ANG-1).
GN ANGPT1 OR AGPT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97134663; PubMed=8980223;

RA Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,
RA Ryan T.E., Bruno J., Radziejewski C., Maisonneuve P.C.,
RA Yancopoulos G.D.;
RT *Isolation of angiopoietin-1, a ligand for the TIE2 receptor, by
RT Cell 87:1161-1169(1996).
RL
CC -1- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS
CC TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
CC PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
CC CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
CC ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
CC VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
CC HEART EARLY DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DEVELOPMENTAL STAGE: EARLY IN DEVELOPMENT. AT E9 TO E11, IT IS
CC ROUND MOST PROMINENTLY IN THE HEART MYOCARDIUM SURROUNDING THE
CC ENDOCARDIUM. LATER, IT BECOMES MORE WIDELY DISTRIBUTED. MOST OFTEN
CC IN THE MESENCHYME SURROUNDING DEVELOPING VESSELS. IN CLOSE
CC ASSOCIATION WITH ENDOTHELIAL CELLS.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U83509; AAB50558.1; -;
CC DR HSSP: P02671; 1FZD.
CC DR MGD: MGI:108448; Agpt.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C; 1.
DR SMART: SM00186; FBG; 1.
DR PROSITE: PS00514; FIBRIN-AG_C_DOMAIN; 1.
KW Glycoprotein; Coiled coil; Signal.
FT SIGNAL 1 19
FT CHAIN 20 498
FT DOMAIN 81 119
FT DOMAIN 153 261
FT DOMAIN 284 498
FT CARBOHYD 92 92
FT CARBOHYD 122 122
FT CARBOHYD 154 154
FT CARBOHYD 243 243
FT CARBOHYD 295 295
SQ SEQUENCE 498 AA; 57505 MM; 285B4FDEC260D800 CRC64;
Query Match 18.6%; Score 391; DB 1; Length 498;
Best Local Similarity 26.7%; Pred. No. 1, 5e-23;
Matches 115; Conservative 67; Mismatches 126; Indels 122; Gaps 16;
QY 23 VQNCVHSHSTDSVYNIVEDGSKNADESKSNDYCKEDCEESCDYKTKITREKHFMCRN 82
DB 115 IQQNAVONHT---ATMLEIGTSLISQT-----AEQTRKLTVEYOVNLQTSRLLEIQL 163
QY 83 LQNSIVSY-----TRSTKILRLNMM 102
DB 164 LENSLSYKLEKOLLQOTNEILKTHEKNSLLEHKLLEMEGKHKEELDTLKEEKENLQGLV 223
QY 103 DEQASLDYLSNOYV-----ELM-----NRVLLLTVEF-----RKQLDPF 138
DB 224 SRQYIIQLELEKQKRNATNNNSVLQKQOELMDVYHNLVNCSTEGVLLKKGKREEKRF 283
QY 139 PRRPVQSHGLDCTDIKDTIGSVTKPSGLYTIHREGSSYPREVNCMDYRGSGWTYQKR 198
DB 284 -----RDCADVY-----QAGFNKSGIYIYINNMPEKPKVCNMDVNGCGWTYIOHR 330
QY 199 IDGIIDFQRLMCDYLDGFGDLGFEWLGKIKFIYVQKNKSFMLYVALBESDPTLAYAS 258
DB 331 EDGSLDFQRGKKEYKMGFGNPSGEYWLGNFIYATISOR--QYMLRIELMDWENRAYSQ 388

```
OY 259 YDNFWLEDETRFKMHLGRYSNAGDAFRGLKEDN--ONAMPFSTVDYDNGCRPAC-- 314
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 369 YDRFHNIGNEKQVRYLXIKGHTGTAG-----KQSSLILHAGDFSRKADNDNCKMKCAL 441
OY 315 LVNGSVSVSCSLHNTKGTWNECGLANLNGIHRS-----GLLTLTGIONGTWTKNNSPV 370
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 442 MLTG-----GWMFDCGSPNLNMGFTAGONHGRKL--NGIKWHYF--KGPSY 484
OY 371 KIKSVSMKR 380
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 485 SURSTTMIR 494

RESULT 10
ID AP2_HUMAN STANDARD: PRT: 496 AA.
AC 015123: QGNRRY:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiopoietin-2 precursor (ANG-2).
GN ANGPT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Lung;
RX MEDLINE=97349327; PubMed=9204896;
RA Maisongier P.C., Surt C., Jones P.F., Bartunkova S., Wiegand S.J.,
RA Padolejewski C., Compton D., McClain J., Aldrich T.H.,
RA Papadopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.;
RT "Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
RT angiogenesis."
RL Science 277:55-60(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=umbilical vein endothelial cells;
RX MEDLINE=20309815; PubMed=10766762;
RA Kim I., Kim J.-H., Ryu Y.S., Jung S.H., Nah J.J., Koh G.Y.;
RT "Characterization and expression of a novel alternatively spliced
RT human angiopoietin-2."
RL J. Biol. Chem. 275:18550-18556(2000).
CC -1- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
CC MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY
CC BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH
CC AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY
CC REDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR
CC REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL
CC CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
CC ANGIOGENIC SIGNAL.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC produced by alternative splicing.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC
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CC
DB EMBL: AF004327; AAB63190.1; -
DB EMBL: AF187858; AAF76526.1; -
DB HSSP: P02671; 1FZD.
DB Genew: HGNC:485; ANGPT2.
DB MIM: 601922; -
DB InterPro: IPR002181; Fibrinogen_C.
DB Pfam: PF00147; Fibrinogen_C; 1.
DB SMART: SM00186; FBG; 1.
```

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DR PROSITE: P500514; FIBRIN_AG_C_DOMAIN; 1.
KW Glycoprotein; Coiled coil; Signal; Alternative splicing;
FT SIGNAL 1 16
FT CHAIN 17 496
FT DOMAIN 130 256
FT DOMAIN 280 496
FT CARBOHYD 89 89
FT CARBOHYD 119 119
FT CARBOHYD 133 133
FT CARBOHYD 151 151
FT CARBOHYD 240 240
FT CARBOHYD 304 304
FT VARSPLIC 97 148
SQ SEQUENCE 496 AA; 56919 MW; 5642A58847A7385C CRC64;

Query Match 18.1%; Score 381.5; DB 1; Length 496;
Best Local Similarity 26.3%; Pred. No. 8.4e-23;
Matches 110; Conservative 73; Mismatches 138; Indels 97; Gaps 16;

OY 23 VQNCVYHSTDSVYNIYVDGSSNADESKSNDYCKEDCEESCDYKTKI---TFREE--- 75
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 112 IQGNAYQNOT-----AMTIGTNLNTQ-----AEQTKLTDVDAOVLNQTTRLEQL 160
OY 76 -RHFMCRN-LQNSIVSYSTRSKL-----LRNMDEQASL 109
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 161 LEHSLSTNKLKQLLDQFSEINKLQDKNSFLKQVLAEMDKHIQLQSIKEKQDLQVLY 220
OY 110 DYLSQVYENLNRVLLT--TEVFRQ-----LDPEHPVQSH 146
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 221 SKQNSTIELEKRIYATATVNNNSVLOKQOHDLMETVNNLLTMNSTNSAKDPVAREQIS 280
OY 147 GLDCTDINKFISVYKTPSGLIYIHPEGSSYFEVYCDMDYGGWYVQKRIIDGIFQ 206
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 281 FBDCAVEFSS-----GHITGITYTLFPNSTEETKAYCDMEAGGGMITIIQREDSSVDR 336
OY 207 RLMCDYLDGFGDLGEFWLGLKRIEYVQKNTSPMLYVALSESDTLAYASYDNFWLED 266
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 337 RTWKREYKVGFGNPSEYVGNFVQSGLTQQR--VYLKILHLKDWGNEASYLSEHFYLS 394
OY 267 ERFRRKMLHGRSSNAGDAFRGLKEDNONAMPFSTVDYDNGCRPACLVNGSQSVKSCSH 326
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 395 EELNRYRIHLKGLTGTAQKI-----SSISQPGNDFSTKQGDNDKNC-----ICKCSQ 439
OY 327 LHNKGTWNECGLANLNGIH-----FSGKLATGIONGTWTKNNSPVKIKSVSMKR 380
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
DB 440 MLT-GWMFDCGSPNLNMGFTAGONHGRKL--NGIKWHY--KSGYSIKATTMIR 492

RESULT 11
FIBR_HUMAN STANDARD: PRT: 491 AA.
AC P02675:
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain precursor (Contains: Fibrinopeptide B).
GN FGB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91344740; PubMed=2102623;
RA Chung D.W., Harris J.E., Davie E.W.;
RT "Nucleotide sequences of the three genes coding for human
RT fibrinogen."
RL Adv. Exp. Med. Biol. 281:39-48(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83283433; PubMed=6688356;
RA Chung D.W., Que B.G., Rixon M.W., Mace M.J., Davie E.W.;
RT "Characterization of complementary deoxyribonucleic acid and genomic
```

RT deoxyribonucleic acid for the beta chain of human fibrinogen.";
 RN Biochemistry 22:3244-3250(1983).
 RP SEQUENCE FROM N.A.
 RA Chung D.W., Harris J.E., Davie E.W.;
 RT "Nucleotide sequences of the three genes coding for human
 RL fibrinogen.";
 RL (in) Liu C.T., Chien S. (eds.);
 RL Fibrinogen, thrombosis, coagulation and fibrinolysis, pp.39-48,
 RL Plenum Press, New York (1991).
 RP SEQUENCE FROM N.A., AND VARIANTS SER-100; HIS-170; LEU-265 AND
 RP LYS-478
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi O.,
 RA Nickerson D.A.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 31-491, AND CARBOHYDRATE-LINKAGE SITE.
 RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
 RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
 RL structural variants.";
 RL (in) Peeters H. (eds.);
 RL Profiles of the biological fluids, Proc. 28th colloquium, pp.51-56,
 RL Pergamon Press, Oxford (1980).
 RN [6]
 RP SEQUENCE OF 31-491.
 RX MEDLINE=79124640; PubMed=420779;
 RA Matt K.W.K., Takagi T., Doolittle R.F.;
 RT "Amino acid sequence of the beta chain of human fibrinogen.";
 RL Biochemistry 18:658-666(1979).
 RN [7]
 RP SEQUENCE OF 31-148, AND DISULFIDE BONDS.
 RX MEDLINE=76225080; PubMed=936108;
 RA Blomback B., Hessel B., Hogd D.;
 RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";
 RL Thromb. Res. 8:639-658(1976).
 RN [8]
 RP SEQUENCE OF 1-38 FROM N.A.
 RX MEDLINE=87146483; PubMed=3029722;
 RA Huber P., Dalmont J., Courtois G., Laurent M., Assouline Z.,
 RA Marguerie G.;
 RT "Characterization of the 5'-flanking region for the human fibrinogen
 RL beta gene.";
 RL Nucleic Acids Res. 15:1615-1625(1987).
 RN [9]
 RP SEQUENCE OF 31-44.
 RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hanton M.;
 RT "Studies on fibrinopeptides from primates.";
 RL Acta Chem. Scand. 19:1788-1789(1965).
 RN [10]
 RP REVIEW, AND DISULFIDE BONDS.
 RX MEDLINE=83254370; PubMed=6575689;
 RA Henschen A., Lottspeich F., Kehl M., Southan C.;
 RT "Covalent structure of fibrinogen.";
 RL Ann. N.Y. Acad. Sci. 408:28-43(1983).
 RN [11]
 RP DISULFIDE BONDS.
 RX MEDLINE=77245999; PubMed=891553;
 RA Gaerlund B., Hessel B., Marguerie G., Murano G., Blomback B.;
 RT "Primary structure of human fibrinogen. Characterization of
 RL disulfide-containing cyanogen-bromide fragments.";
 RL Eur. J. Biochem. 77:595-610(1977).
 RN [12]
 RP DISULFIDE BONDS.
 RA Doolittle R.F., Takagi T., Matt K.W.K., Bouma H. III, Cottrell B.A.,
 RA Cassman K.G., Goldbaum D.M., Doolittle L.R., Friesner S.J.;
 RT "The structures of fibrinogen and fibrin.";
 RL (in) Magnusson S., Ottesen M., Foltmann B., Dano K.,
 RL Neuraath H. (eds.);
 RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172,
 RL Pergamon Press, New York (1978).
 RN [13]
 RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.

RX MEDLINE=84305751; PubMed=6383194;
 RA Doolittle R.F.;
 RT "Fibrinogen and fibrin.";
 RL Annu. Rev. Biochem. 53:195-229(1984).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 164-491.
 RX MEDLINE=97472408; PubMed=9333233;
 RA Spraggon G., Everse S.J., Doolittle R.F.;
 RT "Crystal structures of fragment D from human fibrinogen and its
 RL crosslinked counterpart from fibrin.";
 RL Nature 389:455-462(1997).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 164-491.
 RX MEDLINE=98292395; PubMed=9628725;
 RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
 RT "Crystal structure of fragment double-D from human fibrin with two
 RL different bound ligands.";
 RL Biochemistry 37:8637-8642(1998).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=99175089; PubMed=10074346;
 RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
 RT "Conformational changes in fragments D and double-D from human
 RL fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
 RL Biochemistry 38:2941-2946(1999).
 RN [17]
 RP VARIANT BALTIMORE-2.
 RX MEDLINE=89058942; PubMed=3194892;
 RA Schmeizler C.H., Ebert R.F., Bell W.R.;
 RT "A polymorphism at B beta 448 of fibrinogen identified during
 RL structural studies of fibrinogen Baltimore II.";
 RL Thromb. Res. 52:173-177(1988).
 RN [18]
 RP VARIANT ISE.
 RX MEDLINE=91208409; PubMed=2018836;
 RA Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yamazumi K.,
 RA Asakura S., Shirakawa S.;
 RT "A new congenital abnormal fibrinogen Ise characterized by the
 RL replacement of B beta glycine-15 by cysteine.";
 RL Blood 77:1958-1963(1991).
 RN [19]
 RP VARIANT NAPLES.
 RX MEDLINE=92340664; PubMed=1634610;
 RA Koopman J., Haverkate F., Lord S.T., Grimbergen J., Mannucci P.M.;
 RT "Molecular basis of fibrinogen Naples associated with defective
 RL thrombin binding and thrombophilia. Homozygous substitution of B beta
 RL 68 Ala-->Thr.";
 RL J. Clin. Invest. 90:238-244(1992).
 RN [20]
 RP VARIANTS JUMUIDEN AND NIJMEGEN.
 RX MEDLINE=92228809; PubMed=1565641;
 RA Koopman J., Haverkate F., Grimbergen J., Engesser L., Novakova I.,
 RA Kerst A.F.J.A., Lord S.T.;
 RT "Abnormal fibrinogens Jumuiden (B beta Arg14-->Cys) and Nijmegen (B
 RL beta Arg44-->Cys) form disulfide-linked fibrinogen-albumin
 RL complexes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:3478-3482(1992).
 RN [21]
 RP VARIANT NEW YORK-1.
 RX MEDLINE=85157605; PubMed=3156856;
 RA Liu C.Y., Koehn J.A., Morgan F.J.;
 RT "Characterization of fibrinogen New York 1. A dysfunctional
 RL fibrinogen with a deletion of B beta(9-72) corresponding exactly to
 RL exon 2 of the gene.";
 RL J. Biol. Chem. 260:4390-4396(1985).
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL NODULE.
 CC DIVERGING FROM THIS NODULE ARE 2 THREE-CHAIN COILED COILS, WHICH
 CC CONNECT THE CENTRAL NODULE TO THE DISTAL NODULES CONTAINING THE

Query March	17.8%	Score 375.5	DB 1	Length 491
Best Local Similarity	26.6%	Pred. No. 2.5e-22		
Matches 118; Conservative	56;	Mismatches 142;	Indels 127;	Gaps 17;

RESULT	12	
AGP2_BOVIN		
ID	AGP2_BOVIN	STANDARD;
AC	077802; Q9TSK0;	PRT; 375 AA

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DN      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Angiopoietin-2 (Ang-2) (Fragment).
GN      ANGPT2 OR ANG2.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-Ovary:
RX      MEDLINE=99054348; PubMed=9840613;
RA      Goede V., Schmidt T., Kimmula S., Kozian D., Augustin H.G.;
RT      "Analysis of blood vessel maturation processes during cyclic ovarian
RT      angiogenesis." ;
RL      Lab. Invest. 78:1385-1394(1998).
RN      [2]
RP      SEQUENCE OF 219-355 FROM N.A.
RC      TISSUE-Adrenal cortex;
RX      MEDLINE=98451564; PubMed=9776732;
RA      Mandriota S.J., Pepper M.S.;
RT      "Regulation of angiopoietin-2 mRNA levels in bovine microvascular
RT      endothelial cells by cytokines and hypoxia.";
RL      Citec. Res. 83:852-859(1998).
CC      -1- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
CC      MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY
CC      BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH
CC      AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY
CC      INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR
CC      REGRESSION. IN CONCERT WITH VEGF IT MAY FACILITATE ENDOTHELIAL
CC      CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
CC      ANGIOGENIC SIGNAL.
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- DEVELOPMENTAL STAGE: FOUND TO BE EXPRESSED THROUGHOUT THE OVARIAN
CC      CYCLE. OVEREXPRESSED DURING LUTEOLYSIS. THIS COULD REFLECT THE
CC      REGRESSION OF CAPILLARIES THAT HAD DEVELOPED PERICYTE CONTACT IN
CC      THE MIDSTAGE CORPUS LUTEUM.
CC      -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
-----
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DR      EMBL; AF094699; AAC62450.1; -
DR      EMBL; AF032924; AAC78285.1; -
DR      HSSP; P02671; IEDD.
DR      InterPro; IPR002181; Fibrinogen_C.
DR      Pfam; PF00147; fibrinogen_C; 1.
DR      SMART; SM00186; FBG; 1.
DR      ProSITE; PS00514; FIBRIN_AG_C-DOMAIN; 1.
KW      Glycoprotein; Coiled coil.
FT      NON_TER          1
FT      DOMAIN          10   138    COILED COIL (POTENTIAL).
FT      CARBOHYD         159   375    FIBRINOGEN C-TERMINAL.
FT      CARBOHYD         13     13     N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT      CARBOHYD         31     31     N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT      CARBOHYD        120   120     N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT      CARBOHYD        183   183     N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT      CONFLICT         272   272     S -> L (IN REF. 2).
SQ      SEQUENCE       375 AA; 42761 MW; 6F086C4A5C80050A CRC64;

Query Match           17.8%; Score 375; DB 1; Length 375;
Best Local Similarity 30.2%; Pred.No.1.9e-22;
Matches 112; Conservative 57; Mismatches 136; Indels 66; Gaps 15;

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Db	46	STNKLEQIILPQSTSEISKLQDNKSFLEKVKVLMDKDHIIYQLRISKEEKDQLQVAVSKNS	105
Qy	87	IVSTRS---TKLLIRNMADDEQASLDLYLSNQVNELMNR-----VLLITTE--VFRKOLD	136
Db	106	IIIEELKOLATVATVNNNSVLQKQHDLMETVANNLLTTLTMSNPYSYLAKDEQIIFR---	161
Qy	137	PEPHRPVQSHLDCTDIKOTIGSTYK---TPSGLYIIHPGSSYFPEVMDMDMYRGGWY	193
Db	162	-----DC-----GEAFKSGLTTSGYTLITFPNSTEELKAYADMETGGGWY	202
Qy	194	VIQKRDIGIIDFORLACMDYLDGFDLLGEFFMLGKRTFIYVKNQKTSFMYALLESDDT	253
Db	203	VIQKREDSVDPQRTMKREYKKGFEFNPBSGEHMLGNEPVSQYTGQKR--YVLKILHRDMEGN	260
Qy	254	LAVASYDNFMLEDETRFFKMHILGRTYSGNAGDAFGLAKEDNONAMPSTSDVDNDGCRPA	313
Db	261	EAYSLYDHFVLSNDELNRYRIHLKGLTGAGRI-----SSISQPNDSPTDADNDKC---	312
Qy	314	CLVNGQSVKSCSHLHNKTGMWFNFCGLANLNGIH---FSGKILATIGIOMGTWTKNNSP	369
Db	313	-----ICKCSQMLT-GGMWFADCGPNSNLGMATYIPORQNTNKP--NGIKMYWY--KSGG	360
Qy	370	VKISVSKMIR 380	
Db	361	YSLKATTTMIR 371	

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RESULT 13
AGP2_MOUSE
ID AGP2_MOUSE STANDARD: PRT, 496 AA.
AC 035608;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiopoietin-2 precursor (ANG-2).
GN ANGPT2 OR AGP2.
OS Mus musculus (Mouse).
CC Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=uterus;
RC MEDLINE=97349327; PubMed=9240496;
RX Madsenpiere P.C., Surf C., Jones P.F., Bartunkova S., Wiegand S.J.,
RA Radziejewski C., Compton D.L., McClain J., Aldrich T.H.,
RA Papadopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.;
RT Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
RT angiogenesis."
RL Science 277:55-60(1997).
CC -1- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
CC MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY
CC BE CONTEXT-DEPENDENT. IN THE ABSENCE OF CELL-MATRIX CONTACTS SUCH
CC AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY
CC INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR
CC REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL
CC CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
CC ANGIOGENIC SIGNAL.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY AT SITES OF VASCULAR
CC REMODELING.
CC -1- SIMILARITY: CONTAINS 1 FIRINGEN C-TERMINAL DOMAIN.
CC -----
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CC -----
CC EMBL, AF004326; AAB63189.1; -
CC HSSP; P02671.1;F02D.
CC

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DR	MGD: MG1:1202890; AgpCt.				
DR	InterPro: IPR002181; Fibrinogen_C.				
DR	Pfam: PF00147; Fibrinogen_C; 1.				
DR	SMART: SM00186; FBG; 1.				
DR	PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.				
KW	Glycoprotein; Coiled coil; Signal.				
FT	SIGNAL	1	18	POTENTIAL.	
FT	CHAIN	19	496	ANGIOPOIETIN-2.	
FT	DOMAIN	159	256	COILED COIL (POTENTIAL).	
FT	DOMAIN	280	496	FIBRINOGEN C-TERMINAL.	
FT	CARBOHYD	89	89	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	119	119	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	133	133	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	151	151	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	240	240	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	304	304	N-LINKED (GLCNAC. . .)	(POTENTIAL).
SQ	SEQUENCE	436 AA;	5616 MW;	FA3021FE4E01C410 CRC64;	

Query Match	17.8%;	Score 374.5;	DB 1;	Length 496;
Best Local Similarity	25.5%;	Pred. No. 3e-22;		
Matches 110;	Conservative 72;	Mismatches 125;	Indels 125;	Gaps 16.

Oy	23	VQNGCVHSTEDSSVNVIVEDGSNAKDESKSNDTVCKEDECSDYKTKITREKHFMCRN	82
		: : :	:
Db	112	IQQNVNQNT---AVNIETGTSLLNQTA-----QTAKLTVDGAQVLNQTTRELEQL	160
		---A	---

OY	83	LONSTVSTRSKILLRMMDDEQASLDYLSNOYNELMNRLLLTTEVF-----	131
Dd	161	LHSHL-----STNKLKOLDO-----TSEINKLNKNKSFLFOKVLMDEGHSLOLQ	207
OY	132	-----RKQ--LDPFPHRPV-----OSHGLDCDIDDTIGSVTK--	162
Dd	208	SMEQKDELQVLVSROSSVIDELEKKLVATVNNSLLOKH-----DLMETVNSLTTM	262
OY	163	-----PPSGLIYIHPRGSSYPPEWCMDDMYRGGW	192
Dd	263	SSPNKSSVAIRKEEQTTPRDCAETFEKSGLTTSGLTYTLTFPNSFTEEKACCDMDVGCGW	322
OY	193	TVIQRIGDIIDFOTLMCDYLDFEGDDLGEFWLGKIKFYIVNOKNTSFMLYALASEED	252
Dd	323	TVIQRHREDSVDFOFTWKYEKGEGNPNGEYWLMLNEFYSOLTGGHR--YYLKILKDMWG	382
OY	253	TLVASTYNFMLEDPTRFPFKMHLYGSNNAGDAERGLKKEENQAMFPSISDVNDGCRP	312
Dd	381	NEAHLHYHFPLAGEESNYRIHLGLTGTTAKI-----SSISOGSDSFSTDSPDNDC-	433
OY	313	ACLVNGGQSVKSCSHHNKTGMWFNFECGLANLGIHH-----FSGLATAYGIOMGTWTKNNS	368
Dd	434	-----ICKCSQMLS-GGWHPDACGPSNLNQOITYPOKONTNKF--NGIKRYTW--KGS	482
OY	369	PVKIKSVSMKIR	380
Dd	481	GYSLKATTMMIR	492
 RESULT 14 			
FIBB_RAT			
ID	FIBB_RAT	STANDARD:	PRT: 479 AA.
AC	P14480:		
DT	01-JAN-1990 (Rel. 13, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Fibrinogen beta chain precursor (Contains: Fibrinopeptide.B).		
CN	FCB		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Murida; Murinae; Rattus		
OX	NCBI_taxid:10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Sprague-Dawley; TISSUE=Liver;		
RX	MEDLINE=95143386; Pubmed=7841303;		
RA	Courtney M.A., Buncie L.A., Neroni L.A., Simpson-Haidaris P.J.;		

RT "Cloning of the complete coding sequence of rat fibrinogen B beta
RT chain cDNA: interspecies conservation of fibrin beta 15-42 primary
RT structure.";
RL Blood Coagul. Fibrinolysis 5:487-496(1994).
RN [2]
RP SEQUENCE OF 1-26 FROM N.A.
RX MEDLINE=84194000; PubMed=6232608;
RA Fowlkes D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;
RT "Potential basis for regulation of the coordinately expressed
RT fibrinogen genes: homology in the 5' flanking regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).
RN [3]
RP SEQUENCE OF 19-32.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
RN [4]
RP SEQUENCE OF 183-479 FROM N.A.
RX MEDLINE=89378771; PubMed=2673932;
RA Eastman E.M., Gitula N.B.;
RT "Cloning and characterization of a cDNA for the B beta chain of rat
RT fibrinogen: evolutionary conservation of translated and
RT 3'-untranslated sequences.";
RL Gene 79:151-158(1989).
RN [5]
RP SEQUENCE OF 425-479 FROM N.A.
RC STRAIN-Mistat; TISSUE=Liver;
RX MEDLINE=87134033; PubMed=3817019;
RA Sobczak J., Lotli A.-M., Taroux P., Duguet M.;
RT "Molecular cloning of mRNA sequences transiently induced during rat
RT liver regeneration.";
RL Exp. Cell Res. 169:47-56(1987).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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DR EMBL; U05675; AAA64866.1; -;
DR EMBL; M27220; AAA41160.1; -;
DR EMBL; K01336; AAA98625.1; -;
DR EMBL; M35602; AAA41159.1; -;
DR PIR; A05299; A05299.
DR PIR; PE0010; PE0010.
DR HSSP; P02675; 1FZE.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Blood coagulation; Plasma; Glycoprotein; Signal.
FT SIGNAL 1 18
FT CHAIN 19 479 FIBRINOGEN BETA CHAIN.
FT PEPTIDE 19 32 FIBRINOPEPTIDE B.
FT DISULFID 211 211 INTERCHAIN (WITH THE ALPHA CHAIN)
FT (BY SIMILARITY).
FT DISULFID 215 215 INTERCHAIN (WITH THE GAMMA CHAIN)
FT (BY SIMILARITY).
FT DISULFID 219 304 INTERCHAIN (WITH THE GAMMA CHAIN)
FT (BY SIMILARITY).
FT DISULFID 229 258 BY SIMILARITY.
FT DISULFID 412 425 BY SIMILARITY.

FT CARBOHYD 382 382 N-LINKED (GLUCNA...) (POTENTIAL).
FT CONFLICT 28 30
FT CONFLICT 439 439 L -> Q (IN REF. 5).
FT CONFLICT 441 441 S -> T (IN REF. 5).
FT CONFLICT 445 445 S -> A (IN REF. 5).
FT CONFLICT 467 467 R -> K (IN REF. 5).
FT CONFLICT 475 475 V -> F (IN REF. 5).
SQ SEQUENCE 479 AA: 54303 MW: EC86DB77C3EDEC0 CAC64;
Query Match 17.8%; Score 373.5; DB 1; Length 479;
Best Local Similarity 27.2%; Pred. No. 3.4e-22;
Matches 119; Conservative 49; Mismatches 149; Indels 121; Gaps 15;
QY 25 GNCVHSTDSVYNYVEDGSNAKDESKNDYCKEDCESCVYKRTIREKHFKRNIG 84
DB 81 GGCYHEDGDMVL-----CATGCELRQTLNHE-----RPK 112
QY 85 NSIV-----SYTRSTKLLRNMDQOASLDYLSNOYE----- 118
DB 113 NSIAELNSINIVYETSSVTFQYLLLLKDMKKKQAYADNENVINETSILEDQKLYID 172
QY 119 -----LMNRYLLLTVEFRKQD-----PPHRYQSH-----GLDCTDI 153
DB 173 ETVNDNIPNLRYLSILEDLSKMQKLESDISAQTEYCHTFCTVNCNIPVYSGKECEBI 232
QY 154 KPTIGSVYTPSGLYIINHEGSSYPEEWCMDYRGCGTLYQKRIIDTIDFQRLMCDYL 213
DB 233 IRKGGET-----SEMYLIQDTSKPYRYVCDKTEGTGTIYQNRQDSVDFGRKMDPYK 288
QY 214 DGEFG-----LLGEFMLGIKRTFYLVNKNISFMYLVLESDDTLAAYSDN 261
DB 289 KFGNINATNEDTKYKCGLPGETWLGNDKISQLTRIGPE--LLIEMDKGDKYAHNGC 346
QY 262 FWLEDETRFFKMKHLKRYSGNAGDAF---RGLKEDN---ONAMPFSTDVNDGCRPA 313
DB 347 FTVQFPAANKYQVSVKYNKYGTACNALMEGASOLVGNRTTINGNFFSYTDNDNG---- 402
QY 314 CLVNGOSVKSCHLHNKGTGMFNECGLANLINGIHPSGKL-----LANGIQCTWTK 365
DB 403 -WYTTDPRKQCKR-EDGGGMWYNRCHAMPNGRYWGLYSWMSKNGHTDGVVMWNV-- 458
QY 366 NNSPVKIKSVSKIRMY 383
DB 459 KGSWYSMRMSKIRPVF 476
RESULT 15
FIBG_HUMAN STANDARD. PRT: 453 AA.
AC P02679; P04469; P04470; Q96A14;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen gamma chain precursor (PRO2061).
GN FCG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS GAMMA-A AND GAMMA-B).
RX MEDLINE=85252774; PubMed=2990550;
RA Rixon M.W., Chung D.W., Davie E.W.;
RT "Nucleotide sequence of the gene for the gamma chain of human
RT fibrinogen.";
RL Biochemistry 24:2077-2086(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=8328334; PubMed=6688357;
RA Chung D.W., Chan W.-Y., Davie E.W.;
RT "Characterization of a complementary deoxyribonucleic acid coding for
RT the gamma chain of human fibrinogen.";
RL Biochemistry 22:3250-3256(1983).

[3] SEQUENCE FROM N.A. (ISOFORMS GAMMA-A AND GAMMA-B).
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Peol C.L., Yi Q.,
 RA Nickerson D.A.;
 RN Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE FROM N.A. (ISOFORM GAMMA-A).
 RC Tissue-Fetal liver;
 RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M.,
 RA He F.;
 RT "Functional prediction of the coding sequences of 33 new genes deduced
 RT by analysis of cDNA clones from human fetal liver."
 RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN SEQUENCE FROM N.A. (ISOFORM GAMMA-A).
 RC Tissue-Skeletal muscle;
 RA Strausberg R.;
 RN Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RN SEQUENCE OF 27-437.
 RA Henschen A., Lottspeltch F., Southan C., Topfer-Petersen E.;
 RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
 RT structural variants."
 RL (in) Peeters H. (eds.);
 RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
 RL Pergamon Press, Oxford (1980).
 RN [7]
 RN SEQUENCE OF 75-286 FROM N.A.
 RC Tissue-liver;
 RA MEDLINE-92119334; PubMed-1685103;
 RA Marchetti L., Zaneli T., Malcovati M., Tencini M.L.;
 RT "Polymorphism of the human gamma chain fibrinogen gene."
 RL DNA Seq. 1:419-422(1991).
 RN [8]
 RN SEQUENCE OF 285-437 FROM N.A. (ISOFORMS GAMMA-A AND GAMMA-B).
 RA MEDLINE-85030379; PubMed-6092346; Comeau C.M., Kant J.A.,
 RA Forcace A.J. Jr., Cummings D.E.,
 RT "Structure of the human gamma-fibrinogen gene. Alternate mRNA
 RT splicing near the 3' end of the gene produces gamma A and gamma B
 RT forms of gamma-fibrinogen."
 RL J. Biol. Chem. 259:12826-12830(1984).
 RN [9]
 RN SEQUENCE OF 209-270 FROM N.A.
 RA MEDLINE-84069777; PubMed-6689067;
 RA Iman A.M.A., Eaton M.A.W., Williamson R., Humphries S.;
 RT "Isolation and characterisation of cDNA clones for the A alpha- and
 RT gamma-chains of human fibrinogen."
 RL Nucleic Acids Res. 11:7427-7434(1983).
 RN [10]
 RN SEQUENCE OF 411-453 (ISOFORM GAMMA-B).
 RA MEDLINE-82068993; PubMed-7306501;
 RA Wolfenstein-Todel C., Moessens M.W.;
 RT "Carboxy-terminal amino acid sequence of a human fibrinogen
 RT gamma-chain variant (gamma')." ;
 RL Biochemistry 20:6146-6149(1981).
 RN [11]
 RN REVIEW, AND DISULFIDE BONDS.
 RA MEDLINE-83254370; PubMed-6575689;
 RA Henschen A., Lottspeltch F., Kehl M., Southan C.;
 RT "Covalent structure of fibrinogen."
 RL Ann. N.Y. Acad. Sci. 408:28-43(1983).
 RN [12]
 RN DISULFIDE BONDS.
 RA Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cottrell B.A.,
 RA Cassman K.G., Goldbaum D.W., Doolittle L.R., Friesner S.J.;
 RT "The structures of fibrinogen and fibrin."
 RL (in) Magnusson S., Ottesen M., Foltmann B., Dano K.,
 RL Neurath H. (eds.);
 RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172,
 RL Pergamon Press, New York (1978).
 RN [13]
 RN DISULFIDE BONDS.
 RX MEDLINE-76225080; PubMed-936108;
 RA Blomback B., Hessel B., Hogg D.;
 RT "Disulfide bridges in NH2-terminal part of human fibrinogen."
 RL Thromb. Res. 8:639-658(1976).
 RN [14]
 RN QUATERNARY STRUCTURE, AND DISULFIDE BONDS.
 RX MEDLINE-83231465; PubMed-6860649;
 RA Hoeprich P.D., Doolittle R.F.;
 RT "Dimeric half-molecules of human fibrinogen are joined through
 RT disulfide bonds in an antiparallel orientation."
 RL Biochemistry 22:2049-2055(1983).
 RN [15]
 RN SULFATION.
 RX MEDLINE-91369960; PubMed-1892842;
 RA Farrell D.H., Mulvihill E.R., Huang S., Chung D.W., Davie E.W.;
 RT "Recombinant human fibrinogen and sulfation of the gamma' chain."
 RL Biochemistry 30:9414-9420(1991).
 RN [16]
 RN REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
 RX MEDLINE-84305751; PubMed-6383194;
 RA Doolittle R.F.;
 RT "Fibrinogen and fibrin."
 RL Annu. Rev. Biochem. 53:195-229(1984).
 RN [17]
 RN POLYMERIZATION SITE.
 RX MEDLINE-85014892; PubMed-6592597;
 RA Horwitz B.H., Varadi A., Scheraga H.A.;
 RT "Localization of a fibrin gamma-chain polymerization site within
 RT segment Thr-374 to Glu-396 of human fibrinogen."
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5980-5984(1984).
 RN [18]
 RN POLYMERIZATION SITE.
 RX MEDLINE-81142375; PubMed-6451630;
 RA Oleksa S.A., Budzynski A.Z.;
 RT "Localization of a fibrin polymerization site."
 RL J. Biol. Chem. 256:3544-3549(1981).
 RN [19]
 RN PLATELET AGGREGATION SITE.
 RX MEDLINE-84203545; PubMed-6326808;
 RA Kloczewiak M., Timmons S., Lukas T.J., Hawiger J.;
 RT "Platelet receptor recognition site on human fibrinogen. Synthesis
 RT and structure-function relationship of peptides corresponding to the
 RT carboxy-terminal segment of the gamma chain."
 RL Biochemistry 23:1767-1774(1984).
 RN [20]
 RN PLATELET AGGREGATION SITE.
 RX MEDLINE-84185664; PubMed-6325435;
 RA Plow E.F., Strouj A.H., Meyer D., Marguerie G., Ginsberg M.H.;
 RT "Evidence that three adhesive proteins interact with a common
 RT recognition site on activated platelets."
 RL J. Biol. Chem. 259:5388-5391(1984).
 RN [21]
 RN CALCIUM-BINDING SITE.
 RX MEDLINE-85261382; PubMed-3160702;
 RA Dang C.V., Ebert R.F., Bell W.R.;
 RT "Localization of a fibrinogen calcium binding site between
 RT gamma-subunit positions 311 and 336 by tertium fluorescence."
 RL J. Biol. Chem. 260:9713-9719(1985).
 RN [22]
 RN CHROMATOGRAPHIC COMPARISON OF GAMMA-A AND GAMMA-B CHAINS.
 RX MEDLINE-81054908; PubMed-6933547;
 RA Wolfenstein-Todel C., Moessens M.W.;
 RT "Human plasma fibrinogen heterogeneity: evidence for an extended
 RT carboxyl-terminal sequence in a normal gamma chain variant
 RT (gamma')." ;
 RL Proc. Natl. Acad. Sci. U.S.A. 77:5069-5073(1980).
 RN [23]
 RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.
 RX MEDLINE-97169449; PubMed-9016719;
 RA Yee V.C., Pratt K.P., Cote H.C.F., Je Trong I., Chung D.W.,
 RA Davie E.W., Stenkamp R.E., Teller D.C.;
 RT "Crystal structure of a 30 kDa C-terminal fragment from the gamma
 RT chain of human fibrinogen."

RL Structure 5:125-138(1997).
RN [24] X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.
RX MEDLINE=97352771; PubMed=9207064;
RA Pralt K.P., Cole H.C.F., Chung D.W., Stenkamp R.E., Davie E.W.;
RT "The primary fibrin polymerization pocket: three-dimensional
structure of a 30-kDa C-terminal gamma chain fragment complexed with
the peptide Gly-Pro-Arg-Pro.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:7176-7181(1997).
RN [25] X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 114-432.
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 114-432.
RX MEDLINE=97472408; PubMed=9333233;
RA Spraggon G., Everse S.J., Doolittle R.F.;
RT "Crystal structures of fragment D from human fibrinogen and its
crosslinked counterpart from fibrin.";
RL Nature 389:455-462(1997).
RN [26] X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 114-432.
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 114-432.
RX MEDLINE=98292395; PubMed=9628725;
RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
RT "Crystal structure of fragment double-D from human fibrin with two
different bound ligands.";
RL Biochemistry 37:8637-8642(1998).
RN [27] X-RAY CRYSTALLOGRAPHY.
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=99175089; PubMed=10074346;
RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
RT "Conformational changes in fragments D and double-D from human
fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
RT

Query Match 17.7%; Score 371.5; DB 1; Length 453;
Best Local Similarity 31.9%; Pred. No. 4,6e-22;
Matches 105; Conservative 42; Mismatches 129; Indels 53; Gaps 11;

QY 85 NSIVYSTRSKRLRNMQ-----QASLDYLSNOVNELMNRVLLTTEVFRKQDPF 138
DB 103 NMIDATLTKSRKMLEIKMEASILTHDSIRYLQETVSNNOKIYNLKEKV--AQLEAQ 160
QY 139 PRRP-----VQSH---GLDCTDIKDTIGSVTKTPSGLYITHPEGSYPFEVCMQMDYRGCG 191
DB 161 COEPCKDVTYQIHDIYTKDCQD---IANKAKOSGLYFIKPLKANOQFLYCEIDSGSGNG 216
QY 192 WTVIQKRIDGIDFORLMQDYLDFGFDL---LGEFWLGLKKIFLYVNOKNKTSFMLYVAL 247
DB 217 WTVFQKRIDGSDYFQKKNYIQYKEGFGHLSPTGTTEFWLSEKIHILISTQSAIPYALVEL 276
QY 248 ESEDDTLAVASYDNFMLEDETRFFKMHGKYS-GNAGDAFRGLKED-----NONAM 298
DB 277 EDWNGRTSTADYAMFKVGEADKYRLTYAFAGGDAFGDFGDDPSDKFTSHNGM 336
QY 299 PFSTSDVNDGCRPACLVNGOSVSKSHLHNTGWFNECGLANLNGIHHSGL----- 353
DB 337 OFSTVDNDNDKFEKGCAEDGS-----GWMNKNCHAGHLNGVYYOGGTSKAST 385
QY 354 ---LATGIOMGTWTKNNSPVKIKSVSMKI 379
DB 386 PNGYDNGIIMATW--KTRWYSMKTTMKI 412

Search completed: December 16, 2002, 17:34:39
Job time : 10.2381 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 16, 2002, 17:32:08 ; Search time 29.234 Seconds
(without alignments)
2732.835 Million cell updates/sec

Title: US-09-596-196-4

Perfect score: 2104
Sequence: 1 MMSPSQASLFLNVCIFIG.....PYKIKSVSMKIRMYNPFYK 388

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SP archaea:*
- 2: SP bacteria:*
- 3: SP fungi:*
- 4: SP human:*
- 5: SP invertebrate:*
- 6: SP mammal:*
- 7: SP mnc:*
- 8: SP organelle:*
- 9: SP phage:*
- 10: SP plant:*
- 11: SP rodent:*
- 12: SP virus:*
- 13: SP vertebrate:*
- 14: SP unclassified:*
- 15: SP viirus:*
- 16: SP bacteriap:*
- 17: SP archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	427.5	20.3	652	5	09NDQ1
2	425	20.2	491	4	095841
3	409.5	19.5	357	11	09EPT7
4	404.5	19.2	493	11	09J0J3
5	399.5	19.0	489	13	090218
6	390	18.5	498	6	09BDY8
7	383.5	18.2	308	5	0908M6
8	382	18.2	495	4	09P2Y7
9	380	18.1	346	4	043827
10	379.5	18.0	496	11	09D2D2
11	378.5	18.0	316	5	0908W7
12	378.5	18.0	407	13	09DER1
13	378.5	18.0	488	13	091589
14	378.5	18.0	493	13	09DER2
15	376.5	17.9	441	13	09DER0
16	373.5	17.8	496	6	09BDY7

17	369.5	17.6	220	5	08T8A2	08T8A2 clona savig
18	368.5	17.5	407	13	09PU54	09PU54 gallus gall
19	368.5	17.5	436	4	08WUR3	08WUR3 homo sapien
20	368.5	17.5	436	11	08WCM7	08WCM7 mus musculu
21	368	17.5	314	11	08WC25	08WC25 mus musculu
22	367.5	17.5	337	11	08RIQ3	08RIQ3 mus musculu
23	364.5	17.3	431	6	095L03	095L03 macaca fasc
24	364.5	17.3	513	13	090219	090219 brachydanto
25	364	17.3	341	5	0966W1	0966W1 halocynthia
26	362.5	17.2	435	13	093568	093568 gallus gall
27	360	17.1	356	5	095P98	095P98 halocynthia
28	359	17.1	244	4	09HBP3	09HBP3 homo sapien
29	357.5	17.0	932	13	057587	057587 brachydanto
30	352.5	16.8	592	4	095697	095697 homo sapien
31	352.5	16.8	1294	4	09U0P3	09U0P3 homo sapien
32	352	16.7	324	5	095PA0	095PA0 halocynthia
33	348	16.5	292	5	0908W8	0908W8 tachypieus
34	347	16.5	324	5	095P99	095P99 halocynthia
35	341	16.2	316	6	028529	028529 mustela put
36	339	16.1	712	4	000531	000531 homo sapien
37	339	16.1	1358	4	092752	092752 homo sapien
38	339	16.1	1358	4	015568	015568 homo sapien
39	333.5	15.9	372	5	018545	018545 biophalari
40	333.5	15.9	385	5	0950V9	0950V9 biophalari
41	332.5	15.8	337	6	09BE00	09BE00 macaca fasc
42	330	15.7	1356	11	005546	005546 rattus norv
43	327.5	15.6	235	6	028763	028763 papio cynoc
44	327.5	15.6	1353	13	000546	000546 gallus gall
45	321.5	15.3	440	5	09W291	09W291 drosophila

ALIGNMENTS

RESULT 1

ID	09NDQ1	PRELIMINARY;	PRT;	652 AA.
AC	09NDQ1;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, last annotation update)			
DE	Fibrinogen-like protein.			
GN	CI-FIBRN.			
OS	Clona intestinalis.			
OC	Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;			
OC	Phlebobranchia; Clonidae; Clona.			
OX	NCBI_TaxID=7719;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RA	Hotta K., Takahashi H., Asakura T., Satoh B., Takatori N., Satou Y.,			
RA	Satoh N.;			
RT	*Characterization of Brachyury downstream notochord genes in the Clona			
RT	intestinalis embryo.*;			
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB036849; BAB00626.1; -.			
DR	HSSP; P02671; 1FZD.			
DR	InterPro: IPR002181; Fibrinogen_C.			
DR	Pfam: PF00147; fibrinogen_C; 1.			
DR	SMART; SM00186; FBG; 1.			
DR	PROSITE; PS00514; FIBRIN_AG_C-DOMAIN; 1.			
SQ	SEQUENCE 652 AA; A492BA325162F0E0 CRC64;			

Query Match 20.3%; Score 427.5; DB 5; Length 652;
Best local similarity 30.7%; Pred. No. 1e-26;
Matches 115; Conservative 67; Mismatches 124; Indels. 69; Gaps 16;

QY	50	SKSNDYVCK--EDCESCDYKTKITREKHFV-----CRNLQNSIVSYTR-----	93
DB	293	SOENDDAKAEADYVTFVETDRTVGVQVYEDETQETRSYTRSGVTSRSDYVHNEN	352
QY	94	-----TKLLNNMDEQASL-----DYLNQVN--ELMNRVLLTTEVFRKQL	135
DB	353	EMAFSTTVTHAVEVTPNYISEGCVNIRDGVAITNETGIEFTSRILRAT-----	404

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QY 136 DPFHRPVQSHGL--DCTDIDITIGSVTKTSPGLYIIHPSSSYFEVCMQDIYRGCGWT 193
DB 405 NPTVQDQGTSLPYDCAELV-----ARGVQSGVYDIRP-GTKVWYTCMDPTDGGGWT 459
QY 194 VIKRIGDIIDFORLMDYLDGFGDILGEFWLGLKFIYI-VNOKTSEFMYVALESDD 252
DB 460 MLOGRIDIVFSGKSKYKNGFDINDIHWIGLEKMHISTSKSRMELRLITLMD 519
QY 253 TLAVASDNEFWLEDETRFEFKMLGRYSGNAGDARFGLKKEQNONAMPSTSDVDNDGCRP 312
DB 520 VSHVANGVFIRSEKGNKYOLIAKRYTGTAADAL-NYGENYHHILQPTFTEDRDND----- 574
QY 313 ACIVNGSVKCSHILHNKTMGWFNECGLANLNGIHFGS--KLATGIGOKGTWK----- 365
DB 575 -----GALGNCGRYV-RSGWMFNACFANLNG-NYVYGRKYGVANGIYGTWYKLSDT 627
QY 366 NSPVKIKSVSMKIR 380
DB 628 SNRYSFXYVDMKYR 642

RESULT 2
095841 PRELIMINARY; PRT: 491 AA.
ID 095841
AC 095841
DT 01-MAR-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Angiopoietin Y1 (D595C2.2) (Angiopoietin-related protein 1 precursor).
GN D595C2.2 OR ARP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RX MEDLINE=9148829; PubMed=10025962;
RA Kim I., Kwak H.J., Ahn J.E., So J.N., Liu M., Koh K.N., Koh G.Y.;
RT "Molecular cloning and characterization of a novel angiopoietin family protein, angiopoietin-3."
RL FEBS Lett. 443:353-356(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Cobley V.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Ota T., Nishikawa T., Kawai Y., Suzuki Y., Ishii S., Saito K., Yamamoto J., Sugano S., Isogai T.;
RT "HRI human cDNA sequencing project."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Ito Y., Oike Y., Yasunaga K., Matsumoto S., Ota T., Nishikawa T., Kawai Y., Isogai T., Hamada K., Saito Y., Miyata K., Masuko Y., Suda T.;
RT "Molecular cloning and characterization of novel angiopoietin-related protein (ARP4)."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RX EMBL; AF107253; AAD19608.1;
DR EMBL; AL355520; CAC13169.1;
DR EMBL; AB056476; BAB40691.1;
DR HSSP; P02671; 1FZD.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KM Signal.

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FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 491 POTENTIAL.
SQ SEQUENCE 491 AA; 56719 MW; 3C4DB8DE6CFE7E99 CRC64;

Query Match
Best Local Similarity 26.9%; Score 425; DB 4; Length 491;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

QY 44 SNAKDESKNDIVCKEDSCDVYKTYTRE-EKHFMCRNLONSIVSYTRSTKLLRNMM 102
DB 68 TKGQDASTIKDMITRMDLENLKDVLRSOKREIDVQLVVDVGNIVNEVKLLRKESRMNN 127
QY 103 DE-QQASIDYL-----SNQVNELMNRVLLTTE----- 129
DB 128 SKVTLVWQLHEILIRKDNLSLSOLEKLLNVTTEMLKATRYRELEVKYASLTLDLVN 187
QY 130 -----VFRKQ--LDP-----FPHRPVQSHGL----- 148
DB 188 NQSVMITLLEBQCLRIFFSRQDTHVSPPLVQVYVPHIPIINSQOYTPGLLGNETIQDPGYR 247
QY 149 DCTDIKDTIGSVTKTP-----SGLYIIHPSSSYPREV 181
DB 248 DLMPPDLATSPTKSPFKIPVTFINEGPFKDCQQAKEAGHSVSGIYMIKPPNSGPMQL 307
QY 182 MCDMDYRGCGWTVIQKRIDGITDIFORLMDYLDGFGDILGEFWLGLKFIYIVNOKTSTF 241
DB 308 WCENSLDPCGWTIVIQKRIDGVSYNFFRMWENKKGCGNIDEGWGLLENIMYSNODN--Y 365
QY 242 MLYVALESDDTLAVASDNEFWLEDETRFEFKMLGRYSGNAGDARFGLKKEQNONAMPFS 301
DB 366 KLILIEDMSDKKYVAEYSSFRLEPSEFYRLRLGTIOGNMGDSMM-----HNGKQFT 419
QY 302 TSDVDNDGCRPACIVNGSVKCSHILHNKTMGWFNECGLANLNGIHFGSKLLA---TGI 358
DB 420 TLDRLKD-----WYAGNCAHFH-KGWMYNAACASHNLNGVYGHYRSKHQGI 468
QY 359 QMGWTKNNSPFKIKSVSMKIR 380
DB 469 FWAET--RGSTYSLNAYQVMIK 488

RESULT 3
09EPT7 PRELIMINARY; PRT: 357 AA.
ID 09EPT7
AC 09EPT7
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Prothrombinase FGL2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Rychlik D.F., Chien E., Philippe M.;
RT "FGL2 Expression in the Sprague-Dawley Rat."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF323608; AAG42269.1;
DR HSSP; P02671; 1FZD.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 357 AA; 40966 MW; 31183DD9A02EBBA9 CRC64;

Query Match
Best Local Similarity 32.0%; Score 409.5; DB 11; Length 357;
Matches 121; Conservative 50; Mismatches 150; Indels 57; Gaps 15;
QY 36 VVNIYEDSGSNKDESKNDIVCKEDSCDV--KTKTRREKHMCMNCLNSIVSYTRS 93

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Db      4 VLAEVRLTQAEVADSLKKSCQDCKIQAQAEHPDPGNGAEFTAD-----NNGVQEELESYVK 57
Oy      94 TKKILRRNMDEQA-----SL-----DYLISNOVELLMRRVLLLTTEVER----- 1322
Db      58 LSELKNAKEEIQIGLQGRLESLQLVNNMNNIENYVDKNAMVLTGVNSLSDSKCEKPSQEH 117
Oy     133 KQDPFPHRRPVQSGLDCTDIKDPTIGSVYTKPSGLYIIEEGSSYPREVWACMDIDRGGW 1922
Db     118 NQPNPVQHLIYK----DCSDYY-VLG---KRSSGTATVTPDHRNSSEYVCDMETGGGW 169
Oy     193 TVIKRIRGIDIPFLWCMDYLDGFGDILGFEWTLGKRIEFTVYNQKNSPMLUYALASEDD 2522
Db     170 TVLDARLDGSGINFTRGMKDKYKAGGGLEREFWLGNDKIHILT--KSKEMTLRIDLEDFNG 227
Oy     253 TLAVASYDNFWLDEDETRFEFKMHLRYSAGNAGDAERGLKEDNONAMAFSTDVDNDGCRP 312
Db     228 LTLVAVYDQFVVAHEPLKYLRHLGLNNGYGTAGDALR-PSRHYNHDLRFETTPDDNDNDYPS 286
Oy     313 ACLVNGQSVKSCSHLHNKTKGMWFEEGCLANGLIHH--FSGKILATGIOMGTW--TKNN 367
Db     287 G-----KCG-LYSSSGMWFACIASLNLNGYYNQRYKG--VRNGIFMGTWPGVSQA 3344
Oy     368 SPVKIKSVSMKIRRYNYP 385
Db     335 HPGGKTSFEKFAKMMIRP 352

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RESULT 4			
09JJ03	PRELIMINARY;	PRT;	493 AA.
AC 09JJ03;			
DT 01-OCT-2000 (TREMblrel. 15, Created)			
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)			
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)			
DE Angiogenesis II type 1A receptor associated protein.			
OS Rattus norvegicus (Rat).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX NCBI_Taxid-10116;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN-WISTAR-KYOTO; TISSUE-VASCULAR SMOOTH MUSCLE;			
RA Guo D.F., Baranes D., Ono Y., Porter J.P., Abi-Jaoude E., Orlov S.N.,			
RA Inagami T.;			
RT "AA041 is required for recycling and resensitization of angiotensin II			
RT type 1A receptor.";			
RL Submitted (JUN-1999) to the EMBL/Genbank/DBSJ databases.			
DR EMBL; AF159049; AAR80364.1; -.			
DR HSSP; P02671; 1FZD.			
DR InterPro; IPR002181; Fibrinogen_C.			
DR SMART; PF00147; fibrinogen_C; 1.			
DR Pfam; SM00186; FBG; 1.			
DR Prosite; PS00514; FIBRIN_AG_C_DOMAIN; 1.			
KW Receptor.			
50 SEQUENCE 493 AA; 57159 MW; 7C37652CA472B3341 CRC64;			

Query Match	19.2%;	Score 404.5;	DB 11;	Length 493;
Best Local Similarity	27.1%;	Pred. No. 5.5e-35;		
Matches 108;	Conservative 68;	Mismatches 118;	Indels 105;	Gaps 15;

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07 62 EESDVCVKKIT-----REKHFMICRIONISIVSTYSTKKLNNMDEO--A 107
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 135 KESRMNRNRYQLVMQMLHEIIRKRDNALELSOLENRIIQTADMLQYSKYUDLEHKEQ 184
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
0Y 108 SLDYSINOVNELM-----NRVL--LTTVEVER 132
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 165 HJIDMLAHQSEVIALOEHCORVPARVPORPAPRPVRYQRPYRIIQTISTNEIOS 244
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
0Y 133 KQ----LDP-FPHRPVOSHGDCTDIKDTJISVYKTPSG-----LYII 170
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 245 DONKVLPRPSLTPMALT-----SLPSTDKSGFRRDCLALEHGHSSTSYIV 294
   ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
0Y 171 HPGSSYPEFVACMDMYRGSGMTVIQRIDGIIIDFQILMCDYLDGFGDILLGEFMLGLKKI 230

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Db	295	KPENTNRLMQWCORHDPGGWTVIQRLODSSVNFERNMETYYKQGFENIDGSEWLGLENT	354
Qy	231	FYIVQKTSFPLVYALESEDDTLAYASYNDFLEDETRFEFKHILGRYSNAGDAFRLK	290
Db	355	YWLTVQGN--YKLLVTMEDMSGRKVAFAEYASFRLEPSESEYKLLILGRYHGRAGDSFTW--	410
Qy	291	KEDNQNAPEFSDVDNDNGCRPACLVNGQSVKSCSHLHNTKGMWFNCGLANLNGIHFS	350
Db	411	---HNGKQFTLLDDHD-----VYTG---NCAH-YQKGWVYNAACAHSNLNGVRYRG	455
Qy	351	GKLLA---TGLOMGTWLTNNSPVKIKSVSMKIRRMVNPY	386
Db	456	GHYRSRIQDGVYMAEF--RGGSYSILKTKVMMIRRNPTF	492

RESULT 5			
ID	090218	PRELIMINARY;	PRT; 489 AA.
AC	090218;		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	Angiopietin-2.		
CN	ANG2.		
OS	Brachydanio rerio (Zebrafish) (Zebra danio).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;		
OC	Cyprinidae; Danio.		
OX	NCBI_TaxID=7955;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21391693; PubMed=11500985;		
RA	Pham V.N., Roman B.L., Weinstein B.M.;		
RT	"Isolation and expression analysis of three zebrafish angiopoietin		
RT	genes.";		
RL	Dev. Dyn. 221:470-474(2001).		
DR	EMBL: AF379603; AA83348.1; -.		
DR	InterPro: IPR002181; Fibrinogen_C.1.		
DR	Pfam: PF00147; Fibrinogen_C.1.		
DR	PROSITE: PS00514; FIBRIN_AG_C.DOMAIN; UNKNOWN.1.		
SO	SEQUENCE 489 AA; 55785 MW; 3ABAEE6278539B33C CRC64;		

Query Match	19.0%;	Score 399.5;	DB 13;	Length 489;
Best Local Similarity	28.1%;	Pred. No. 1.4e-24;		
Matches 114;	Conservative 55;	Mismatches 131;	Indels 105;	Gaps 16

[illegible]

Db 427 -SCKCAQMATGGMWFEACGPSNLNGIYSGNSVNIYNSIKMYW 470

RESULT 6

Q9BDY8 PRELIMINARY; PRT; 498 AA.

AC Q9BDY8; 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Angiopoietin 1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21153163; PubMed=11230987;
RA Kim I., Moon S.O., Han G.Y., Pak Y.K., Moon S.K., Kim J.J., Koh G.Y.;
RT "The angiotensin-II type 2 system in coronary artery endothelium prevents
oxidized low-density lipoprotein-induced apoptosis.";
RL Cardiovasc. Res. 49:872-881(2001).
DR EMBL; AF233227; AAK14992.1; -.
DR HSSP; P02671; 1FZD.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 498 AA; 57413 MW; 8A01C8EF56061876 CRC64;

Query Match 18.5%; Score 390; DB 6; Length 498;
Best Local Similarity 26.7%; Pred. No. 8.7e-24;

Matches 115; Conservative 66; Mismatches 127; Indels 122; Gaps 16;

QY 23 VQNCVHSTDSVYVIEDGSSNANDESKSNDTVCKEDCESDVKTKITREKHPMCRN 82
Db 115 IQQNAVQNHNT-----ATMEIGTSLLSQT-----AEQTRKILDTVETQVINGSRLEIQ 163
QY 83 LQNSIVSY-----TRSTKLLRNMM 102
Db 164 LENSLSITYLEKQQLQOTNEILKHEKNSLLEKHLIEMEGKHELDTLKEKENLQGLV 223
QY 103 DEQQASLDYLSNQVN-----ELM-----NRVLLTTEYF-----RKOLDFE 138
Db 224 TQGTITIQLEKQLNRATNNNSVLQKQLELMDYVNLNLTCTKEVLLKGGKEEVKRF 283
QY 139 PRRPVQSHGLDCTDIKDTIGSVTKTPSGLYIHPREGSSYPFEVMDMDYRGSGWTVIQKR 198
Db 284 -----RDCADYV-----QAGFNKSGIYTIYINNMPREPKVFCNMDLNGSGWTVIQHR 330
QY 199 IDGIIDFQRLMCDYLDGFGDLLGEFPLGLKTFIYVNOKNTSFMILYVALESEDDTLAVAS 258
Db 331 EDGSLDFQGMKEVYKMGFGNPSGFTWLGNEFLFATTSQR--OYTLTELTMDWGNRAVYSQ 388
QY 259 YDNFMLEDETREFKMHILGRYSNAGDAFGLKEDN--ONAMPFSTVDVNDGCRPAC-- 314
Db 389 YDRFHIGNKQVRYLYLAKHSGTAG-----KQSLILHAGDFSTKDDNDNCKKCAL 441
QY 315 LVNGQSVKSCSHLHNKTGGMWFEACGGLANINGIHPS---GKLLATGIQMGWTKNNSPV 370
Db 442 MLTG-----GWMFDCAGPSNLNGMFEYTAGQNHGKL--NGIKWHF--KGPSY 484
QY 371 KIKSVSMKIR 380
Db 485 SURSTYMMIR 494

RESULT 7

Q9UBW6 PRELIMINARY; PRT; 308 AA.

AC Q9UBW6; 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)

DE Tachylectin-5b isoform.
OS Tachypneus tridentatus (Japanese horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachypneus.
OX NCBI_Taxid=6853;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93398666; PubMed=10468566;
RA Gokudan S., Muta T., Tsuda R., Koort K., Kawahara T., Seki N.,
RA Mizunoe Y., Wai S.N., Iwanaga S., Kawabata S.;
RT "Horseshoe crab acetyl group-recognizing lectins involved in innate
immunity are structurally related to fibrinogen.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10086-10091(1999).
DR EMBL; AB024739; BAA84190.1; -.
DR HSSP; P02671; 1FZD.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 308 AA; 35136 MW; 36161E65EE77E0BF CRC64;

Query Match 18.2%; Score 383.5; DB 5; Length 308;
Best Local Similarity 29.5%; Pred. No. 1.6e-23;

Matches 114; Conservative 45; Mismatches 116; Indels 111; Gaps 15;

QY 9 LFLVNCIFICGFEVQNCVH-----STDSVYVIEDGSSNANDESKSNDTVCKEDCES 64
Db 8 LFLCYSLVLVAGD-----VHHNACSTVCSLKGIDVSDTLDLAKER----- 50
QY 65 CVKRTITREKHEKFMCRNLQNSIVSTYRSTKLLRNMMDEQASLDYLSNQVNLNRYL 124
Db 51 -----LATLQNSISCKDKAF-----YMEYTYVNTQNK-- 77
QY 125 LLTTEVFRKOLDFPFRPVQSHGL--DCTDIKDTIGSVTKTPSGLYIHPREGSSYPFEV 182
Db 78 -----AEKNGLPINC-----TYVQGNRRISGIMYPLNHPISYF 115
QY 183 CDMYRGSGWTVIQKRID---GIIDFQRLMCDYLDGFGDLLGEFPLGLKTFIYVNOKNT 239
Db 116 CDMETAGGWTYVQIRGDRGQPIQNFYQWESYKNGFNLTEFEWGLNDIIFVLQNG--D 173
QY 240 SFMLYVALESEDDTLAVASVNDNFLEDETRFPMHILGRYSNAGDAFRLKEDNAMP 299
Db 174 SYVLRYLDEDFEGRRYAEVFEFLVSEIETLYKMSKTYTKGDGDSL-----SOHNNP 227
QY 300 FSTSDVNDGCRPACLVNGQSVKSCSHLHNKTGGMWFEACGLANLNGI-----HHFSGKLL 354
Db 228 FTTKRDND-----KMEKNCAEAL--KGSWMYNACHSHSLNGLNGLRGHIES----- 272
QY 355 ATGIQMGWTKNNSPVKIKSVSMKIR 380
Db 273 AVGVNMYQWRGHVSLKVS--EWMKIR 296

RESULT 8

Q9P2Y7 PRELIMINARY; PRT; 495 AA.

AC Q9P2Y7; 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Angiopoietin-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homalidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99126459; PubMed=9927494;
RA Tanaka S., Mori M., Sakamoto Y., Makuuchi M., Sugimachi K.,
RA Wands J.R.;

RT "Biologic significance of angiotensin-2 expression in human

RT hepatocellular carcinoma.
 RL J. Clin. Invest. 103:341-345(1999).
 DR EMBL: AB009865; BAA95590.1;
 DR HSSP: P02671; IFZD.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C; 1.
 DR SMART: SM00186; FIB; 1.
 DR PROSITE: PS00514; FIBRIN_AG_C-DOMAIN; 1.
 SQ SEQUENCE 495 AA; 56848 MW; EBFAC35ABF1F08P6 CRC64;

Query Match 18.2%; Score 382; DB 4; Length 495;
 Best Local Similarity 26.4%; Pred. No. 3.9e-23;

Matches 110; Conservative 73; Mismatches 138; Indels 96; Gaps 16;

QY 23 VQNCVHSTDSVYNIIVEDGNADESKSNDTVCKEDCEESCDVKTIT-
 DB 112 IQQAAVGNQF---AVNIEIGTNLNGT-----AQGTRLDYVEAVALNGTRLEQL 160
 QY 76 -KHEMCN-IONSVSTRSTKTL-----LNRMDEQOASL 109
 DB 161 LEHSLSTNKEKQILDOTSEINKLQDRNSFLEKKVLAEMDKHIIQLQSIKEEKDQLAVLY 220
 QY 110 DYLSNOYNEIMNRYLLT--TEVERKO-----LDPRHRPVQSHG 147
 DB 221 SKONSTIELEKKIVTATVNNNSVLQKQOHLMETVNNLLTMSTNSKDPYVAEEQISF 280
 QY 148 LDCTDINDIGSVTKPTSGYLIHPEGSSYPFEVCMQMDYRGSGVTYQKRIDGIIDFOR 207
 DB 281 RDCAEVEKRS---GHTNGIYTLTFPSTBEIKAYCDMEAGCGWTIIQREDSVDPQR 336
 QY 208 LMCYDLDGFQDLGEFNLGKIKIYIVNOKNTSPMLYVALESDDTLAYASYNFWEDE 267
 DB 337 TWKEYKGFGEFNPSEYMLGNFVSQTLNQOR--YVLKIHLMQWEGNEAYSLYEHFYLSSE 394
 QY 268 TRFCKMLGRYSNAGAFRGKEDKEDNONAMPSTSDVNDGCRPACLYNQSVKCSHL 327
 DB 395 ELNRIHLKGLTGAGKI-----SSISOPGDSFTKGDNDKNC-----ICKCSQM 439
 QY 328 HNKGTWPFNECGLANGLNHIH---FSQKLTATGIOMGTWTKNNSPVKIKSVSKIR 380
 DB 440 LT-GGMWFDACGPFNLNOMYYPQORNTNKF--NGIKMYW--KSGYSLKATYTMIR 491

RESULT 9

043827 PRELIMINARY; PRT; 346 AA.

AC 043827;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE CDP6 (Angiopoietin-1-like factor) (CDP6 protein).
 GN DJ647M16.1 OR CDP6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC SEQUENCE FROM N.A.
 RA TISSUE=CORNEA;
 RA Peek R., van Gelderen B.E., Bruinenberg M., Kijlstra A.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RC SEQUENCE FROM N.A.
 RA Bagutley C.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RC SEQUENCE FROM N.A.
 RA TISSUE=SKIN;
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RC SEQUENCE FROM N.A.
 RA MEDLINE=21318995; PubMed=11426320;

RA Stover C., Endo Y., Takahashi M., Lynch N., Constantinescu C.,
 RA Vorup-Jensen T., Thiel S., Friedl H., Hankeln T., Hall R., Gregory S.,
 RA Fujita T., Schwaebler W.;
 RT "The human gene for mannin-binding lectin-associated serine protease-2
 RT (MASP-2), the effector component of the lectin route of complement
 RT activation, is part of a tightly linked gene cluster on chromosome
 RT 1p36.2-3."
 RL Genes Immun. 2:119-127(2001).
 DR EMBL: Y16132; CAAT6078.1;
 DR EMBL: AL049653; CAB44734.1;
 DR EMBL: BC001881; AAH01881.1;
 DR EMBL: AJ300188; CAC15571.1;
 DR HSSP: P02671; IFZD.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C; 1.
 DR SMART: SM00186; FIB; 1.
 SQ SEQUENCE 346 AA; 40018 MW; AEC0A601CC498B43 CRC64;

Query Match 18.1%; Score 380; DB 4; Length 346;
 Best Local Similarity 27.9%; Pred. No. 3.6e-23;

Matches 107; Conservative 67; Mismatches 138; Indels 72; Gaps 15;

QY 14 VCITFCGEVQNCVHSTDSVYNIIVEDGNADESKSNDTVCKEDCEESCDVKTIT- 72
 DB 12 LCIFIVAFV-----SHPAWLKLSKHKTPAPQPLKAAN--C--CEEVKEIKAAVAN 58
 QY 73 -----BEKHEMCN-IONSVSTRSTKTLRNRMDEQOASLDYLSNOYNEIMNR 122
 DB 59 LSSLSELNKQGEKDWVSVMQ---VMELENSKRMEERLIDASKSEEMNQDIDMQL 115
 QY 123 VLLITTEVERKQDLFPFHRPVQSHGLDCTDIKD--TIGSVTKPTSGYLIHPEGSSYPF 179
 DB 116 AAQVYVTSADAI-----YDCSSLYOKNRYRISGYKLPDPDFLSPF-----L 158
 QY 180 EVMCDMDYRGSGVTVYQKRIDGIIDFORLNCDDYLDGPFQDLGEFNLGKIKIYIVNOKNT 239
 DB 159 EVFCDMETSGGGWTIIQKRGSLVSFYDMQYKRGFGSISGDPLGHEHJHRSRQPT- 217
 QY 240 SFMLYVALESDDTLAYASYNFWEDETRPFKMLHGRYSNAG--DAPRGKEDKEDNONAM 298
 DB 218 --RLRVEKEDMEGNIRAYEASHFVYGNELNSYRLFGLGYTGNVGDALQ-----YHNNT 269
 QY 299 PFSTSDVNDGCRPACLYNQSVKCSHLHNKGTGWFNECGLANGLIHPSGK--LLAT 356
 DB 270 AFSTRKDKNDNC-----LDKCAQL--RKGGYWCCTDSNLNGYYRLGHEHNKHL 318
 QY 357 GICMGTWTKNNSPVKIKSVSKIR 380
 DB 319 GITWYGM--HGSTYSLKRVEMKIR 340

RESULT 10

09D2D2 PRELIMINARY; PRT; 496 AA.

AC 09D2D2;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE 11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length
 DE enriched library, clone:5031400E18, full insert sequence (Angiopoietin
 DE 2).
 GN AGPT2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J; TISSUE=OVARY, AND UTERUS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Pletschmann W., Gaasterland T., Gissi C., King B., Kochava H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikola I., Pesole G., Quackenbush J.,
RA Schiraldi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli P., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., But C., Fletcher C., Fujita M., Gariboldi M.,
RA Guellinich S., Hill D., Holmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shiba Y., Storch K.-F.,
RA Suuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszewski A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
RP [2]
RA STRAUBER R.;
RA Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK019860; BAB1887.1; -
DR EMBL; BC027216; AAH27216.1; -
DR HSSP; P02671; 1FZD.
DR MGD; MGI:1202890; Agpt2.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 496 AA; 56575 MW; E7563B498A0EF331 CRC64;

Query Match 18.0%; Score 379.5; DB 11; Length 496;
Best Local Similarity 25.7%; Pred. No. 6.3e-23;
Matches 111; Conservative 71; Mismatches 125; Indels 16; Gaps 16;

QY 23 VQGNVHSTDSVYNIEDGSSNAKDESKNDYCKEDCEESCDYKTKTRREKHFMCN 82
DB 112 IQGNVYVQNT---AVMEIGTSLNQTAA-----QTRKLTVEAGVQLNTRHEQL 160
QY 83 LQNSVSTRSTKLLRNMDQASLDYLSNQVNEMLNRVLLTTEVF----- 131
DB 161 LQHSI---STNKLKQILDQ-----TSEINKLNKNSFLBQKVLDMGKHSQQL 207
QY 132 -----RKO-----LOFPHRPV-----QSHGLDCTDIDKDTIGSVTK-- 162
DB 208 SMKEQKDELQVLYVSKSSYIDLEKLLVATVYNSNLLQKQH-----DLMETVNSLLTMM 262
QY 163 -----PPSGLYIIHPGSSSYPFEEWCMQMDYRGGM 192
DB 263 SSPNSKSSVAIRKEQOTFRDCAELFKSGLTSGIYTLFRPSTBEIKAYCDMDYGGGM 322
QY 193 TVIQRRIGIIDFORLKCDDYLDGFGDLLGEFVLGLKIFYIVNQKNTSEMLVALESEDD 252
DB 323 TVIQHREGSDVDFORTWKEKGEFGSPGLGEYWLGNDFVSQLTGQHR--YVLKIQLKDMGK 380
QY 253 TLAVSYDNFMEDFTREFKMLGRYSGNAGDAFRGLKKEQNMAMPSTVDNDGCRP 312
DB 361 NEAHSLLDHFYIAGESSNRIHLTGLTGAGKI-----SSISOPGSDSTKDSNDK-- 433
QY 313 ACLVNGSVKSCSHLNKTKGMFNEGCLANLNGIH-----FSGKLLATGICMGVTKNNS 368
DB 434 -----ICKCSQMLN--GGMWFADACPSNLNGQYYPQKQNTNKP--NQIKYIY--KGS 480
QY 369 PVKIKSVSMKIR 380
DB 481 GYSLKATMTMIR 492

DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
DE Tachylectin-5B.
OS Eukaryotes; Tridactylus (Japanese horseshoe crab).
OC Tachylectin; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachylectus.
OX NCBI_TaxID=6853;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9398666; PubMed=10468566;
RA Gokudan S., Muta T., Tsuda R., Koori K., Kawahara T., Seki N.,
RA Mizuno Y., Wai S.N., Iwanaga S., Kawabata S.;
RT "Horseshoe crab acetyl group-recognizing lectins involved in innate
RT immunity are structurally related to fibrinogen";
RT Proc. Natl. Acad. Sci. U.S.A. 96:10086-10091(1999).
DR EMBL; AB024738; BAA84189.1; -
DR HSSP; P02671; 1FZD.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 316 AA; 36112 MW; 6FEBED4159EDFID CRC64;

Query Match 18.0%; Score 378.5; DB 5; Length 316;
Best Local Similarity 29.3%; Pred. No. 4.2e-23;
Matches 113; Conservative 45; Mismatches 117; Indels 11; Gaps 15;

QY 9 LFLNCFICEGVVQGNVNH-----STDSSVYNIEDGSSNAKDESKNDYCKEDCEES 64
DB 16 LFLNCFISLVAD-----VHHNAACSTVCSLKGILDSVLDLAKER----- 58
QY 65 CVKTKRITREKHFMCNINQNSIVSTRSTKLLRNMDQASLDYLSNQVNEMLNRVLL 124
DB 59 -----LATLQNPICSKDAF-----YMETVYVQNK-- 85
QY 125 LITTEVFRQLDPPHRRPQVSHGL--DCTDIDKDTIGSVTKTPSGLYIIHPGSSYPFEEW 182
DB 86 -----AEKNGLPINCA-----TYQGNKRTSGITMPLFLNHRISVF 123
QY 183 CDMYRGGMVYIQRID--GIIDFORLKCDDYLDGFGDLLGEFVLGLKIFYIVNQKNT 239
DB 124 CDMETAGGGMVYIQRIDGRCPIQNFQWESYKNGFNLTFEPLGNDIIVLNQ--D 181
QY 240 SFMLYVALESEDDTLAYASYDNFMLEDFTREFKMLGRYSGNAGDAFRGLKKEQNMAMP 299
DB 182 SYVLRLVDEDFGGRYAVAFVLRSEIETLYKMSFKTYKGDAGDSL-----SOHNNMP 235
QY 300 FSTSDVNDGCRPACLVNGSVKSCSHLNKTKGMFNEGCLANLNGI-----HHSGLK 354
DB 236 FTTKDRND-----KWEKNCABAY--KGMWYNACHNSNLGMVLRGPHRES---- 280
QY 355 ATGIQMGVTKNNSPVKIKSVSMKIR 380
DB 281 AVGVNMWQYGRGHNSLAKVS--EMKIR 304

RESULT 12
Q9DER1 PRELIMINARY; PRT; 407 AA.
ID Q9DER1
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Angiopoietin-2B.
GN ANGIOPOIETIN-2B.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20422311; PubMed=10964717;

RA Mezquita J., Mezquita P., Montserrat P., Mezquita B., Francone V.,
 RA Villagrasa X., Mezquita C.;
 RT "Genomic structure and alternative splicing of chicken angiopoietin-
 2.";
 RL Biochem. Biophys. Res. Commun. 275:643-651(2000).
 DR EMBL: AJ289778; CAC08175.1; -.
 DR HSSP: P02671; 1F2D.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C; 1.
 DR SMART: SM00186; FBG; 1.
 DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
 SQ SEQUENCE 407 AA; 46687 MW; 8863BA0AB8C7A41C CRC64;

 Query Match 18.0%; Score 378.5; DB 13; Length 407;
 Best Local Similarity 26.4%; Pred. No. 5.9e-23;
 Matches 112; Conservative 68; Mismatches 135; Indels 109; Gaps 17;

 QY 23 VQGCNHHSSVYNNIVDEGSMNKKDESKNDYCKEDCESGVKRTITEEHKFMKN 82
 DB 23 IQGTAVONQ---AVMIEGTNLNQT-----AEQTRKLTVEAQLNQTRELQL 71
 QY 83 LQNSIVSTSTKTLR-----NMDEQASLDYLSNOVNL----- 119
 DB 72 LEHSL-----STNLEKQISVQTEITKLOEKNFLEKRVLEMEDKHTLOLSIKDEKQ 126
 QY 120 -----MNRVL-----LITTEVFRKQLODPFHPVQS-HGL----- 148
 DB 127 LQVLVAHONSIELEKQLVATVANSVYLQKQHDLMETVHNLMTSPNSAKKNFLAK 186
 QY 149 -----DCID-IDKDTIGSYTKTPSGLYIHPGSSYFPEVMCDMDYRGGWYIQRID 200
 DB 187 EEOISFDCAEAFKSGL-----TTSGLYTLTFPNSAQEKKAYCMESNGGWTYLOQRD 241
 QY 201 GIIDFQRLMCDYLDGFDLGEFWLGLKPIFYIVNOKTSPMLVVALESDDTLAYASYD 260
 DB 242 GSVDFHTWKEKIGFEDPAGETWLGNEFVSQLTNQR--YVLKILKDMEGNAIYITID 299
 QY 261 NFWLEDTREFFKMHLGRYSNAGDAFRGLKEDNQNAPESTDVNDGCRPAQLVNGQS 320
 DB 300 QFYLANEOKRYRIHLKLTGTAGK-----SSISQPCNDFSTKADNDKC----- 344
 QY 321 VKSSHLNHTGWMENSCGLANLNGIH---FSGKLLANGIOWGTYTKNNSPKIKSVS 376
 DB 345 ICKSSQMLT-GGWEDACGSPNLNGMYTPLRQNNK--NGIKWYV--KSGYSLKATY 399
 QY 377 MKIR 380
 DB 400 MMIR 403

 RESULT 13
 Q91589 PRELIMINARY; PRT; 488 AA.
 ID 091589
 AC 091589: 091546:
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE Fibrinogen B-beta subunit precursor.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodidae; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=95369693; Pubmed=7642099;
 RA Roberts L.R., Nichols L.A., Holland L.J.;
 RT "cDNA and amino-acid sequences and organization of the gene encoding
 the B beta subunit of fibrinogen from Xenopus laevis.";
 RL Gene 160:223-228(1995).
 RN [2]
 RP SEQUENCE OF 1-25 FROM N.A.

RX MEDLINE=94032285; Pubmed=8218230;
 RA Roberts L.R., Nichols L.A., Holland L.J.;
 RT "Transcriptional regulation of the Xenopus laevis B beta fibrinogen
 RT subunit gene by glucocorticoids and hepatocyte nuclear factor 1:
 RT analysis by transfection into primary liver cells.";
 RL Biochemistry 32:11627-11637(1993).
 RN [3]
 RP SEQUENCE OF 1-25 FROM N.A.
 RA Holland L.J.;
 RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U19618; AAA85283.1; -.
 DR EMBL: U05035; AAA60463.1; -.
 DR HSSP: P02675; 1F2G.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C; 1.
 DR SMART: SM00186; FBG; 1.
 DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
 KW Signal.
 FT SIGNAL 1 16
 FT CHAIN 17 43 B FIBRINOPEPTIDE.
 FT CHAIN 17 488 FIBRINOGEN B-BETA SUBUNIT.
 SQ SEQUENCE 488 AA; 54803 MW; 660E03844B6C6414 CRC64;

 Query Match 18.0%; Score 378.5; DB 13; Length 488;
 Best Local Similarity 28.6%; Pred. No. 7.5e-23;
 Matches 115; Conservative 49; Mismatches 143; Indels 95; Gaps 15;

 QY 61 CEESDVYKTKTBREKH-----MCRNLQNSIVSTSTKTLRNMMDQOASLDY 111
 DB 106 CPTGCELFTLLKQERNVKTAINDRGRVETLAOSANNVYTYVGLGKIENQOQTLDN 165
 QY 112 LSNQVNL-----MNRVLLITTEVFRKQLODPFHPR----- 141
 DB 166 -QNVVNEVNELEBQYTFIKNDIKPISNRILROVLENRSKIQKLETAIOVENC 224
 QY 142 -----PQSHGLDCTDKDTIGSYTKTPSGLYIHPGSSYFPEVMCDMDYRGGW 192
 DB 225 SPCVYTPPIPVVS-GKEEEIYRRGGT-----SEWYLIQPSFPRFVYCDMAITHDGM 279
 QY 193 TVICKRIGIIDFQRLMCDYLDGFG-----DLGGEFWLGLKPIFYIVNOKNFS 241
 DB 280 TVIQNRQDGSVGFRTWDSYSGFNIAANGKIGICDMPGEFWGNEKTSQLTNIGATEA 339
 QY 242 MLYVALESDDTLAYASYDNFWLEDTREFFKMHLGRYSNAGDAFRG---LKKEDN--- 294
 DB 340 LF--EMEDWDGAKYTAQYTGFTVQNEANKYOLSVGYGTAGNMLMOSASOLKGENRMT 397
 QY 295 -QNAPESTDVNDGCRPAQLVNGQSVKCSHLHNKGTWPFNECGLANLNGIHFGSKL 353
 DB 398 IHNGMFSTFDNDGQWQ---HSDPNKQCSK-EDGGGWMYNRCHAMPNGRYWGGY 451
 QY 354 -----LATGIOWGTYTKNNSPKIKSVSMKIRMYNPEF 387
 DB 452 TWDMAKHGTDGQVVMNM--KDSWYSMKKMSIKIR---PYF 487

 RESULT 14
 Q9DER2 PRELIMINARY; PRT; 493 AA.
 ID 09DER2
 AC 09DER2:
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Angiopoietin-2.
 GN ANGIOPOIETIN-2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20422311; Pubmed=10964717;

RA Mezquita J., Mezquita P., Montserrat P., Mezquita B., Franccone V.,
 RA Villagrosa X., Mezquita C.,
 RT "Genomic structure and alternative splicing of chicken angiotensin-
 2."
 RL Biochem. Biophys. Res. Commun. 275:643-651(2000).
 DR EMBL; AJ289777; CAC08174.1; -.
 DR HSSP; P02671; 1FZD.
 DR InterPro; IPR002181; Fibrinogen_C.
 DR Pfam; PF00147; Fibrinogen_C; 1.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN-AG_C_DOMAIN; 1.
 DR SEQUENCE 493 AA; 56393 MW; B0JA21F90172P6DA CRC64;

Query Match 18.0%; Score 378.5; DB 13; Length 493;
 Best Local Similarity 26.4%; Pred. No. 7.6e-23;
 Matches 112; Conservative 68; Mismatches 135; Indels 109; Gaps 17;

QY 23 VQGNVHSTDSVYVNIIVEDGSDNADESKNDYCKEDCESCDVYTKITREKHKMCHN 82
 DB 109 IQOTAVQNOT-----AVMIEIGTNLNGT-----AEQTRKLTVDYNAQVNLQTTTLEQL 157
 QY 83 LQNSIVSYTRSTKTLR-----NMDEQOASLDYLSNOVNL----- 119
 DB 158 LEHSL-----STNKLEROISVQTNETTKLOEKNFLEKHYLEMDKHTLQLKSIDKEDQ 212
 QY 120 -----MNRVL-----LLTTEVFRKQLDPRPRVOS-HGL----- 148
 DB 213 LQVLYARQNSITIELEKQVLTATVNNNSVLOKQOHDLMETVHNLTIMSTPNSAKKNFIK 272
 QY 149 -----DCTD-IKDTIGSVTKTPSGLYIHPGSSYPFEVCMQDYGSGWTVIQRI 200
 DB 273 EQGISPKDCAEAFKSGL-----TTSGLYTLTFPNSAQEKAKACDMNSNGGWTVLORRD 327
 QY 201 GIIDPQRLMCDYLDGFDLGERFWLGKIKIFYVNOKNTSFMLYVALESDDTLAYASD 260
 DB 328 GSVDPHRTWKYKIGFGDPAGEYWLGNFEVSQLTNQR--YVLKILKMEGNEATLYD 385
 QY 261 NWLEDETFEPMHIGRYSGNAGDAFRGLKEDNQAMPEFSTVDVNDGCRACLVNGOS 320
 DB 386 QFYLANEEOKTYRIHLKGLGTAGKI-----SSISQPNDFSTKDDADNDKC----- 430
 QY 321 VNSCSHLNKTGMFNECGLANLNGIHH---FSGKLATGICQWGTWTKNNSPVKIKISVS 376
 DB 431 ICKGSOMLT-GGWMFPDAGCPSNLNGWYPLRQNNKF--NGIKWYV--KSGYSILKATT 485
 QY 377 MKIR 380
 DB 486 MMIR 489

RESULT 15

Q9DERO PRELIMINARY: PRT; 441 AA.
 AC Q9DERO;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
 DE Angiotensin-2C.
 GN ANGIOPOIETIN-2C.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus
 CX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20422311; PubMed=10964717;
 RA Mezquita J., Mezquita P., Montserrat P., Mezquita B., Franccone V.,
 RA Villagrosa X., Mezquita C.,
 RT "Genomic structure and alternative splicing of chicken angiotensin-
 2."
 RL Biochem. Biophys. Res. Commun. 275:643-651(2000).
 DR EMBL; AJ289779; CAC08176.1; -.

DR HSSP; P02671; 1FZD.
 DR InterPro; IPR002181; Fibrinogen_C.
 DR Pfam; PF00147; Fibrinogen_C; 1.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN-AG_C_DOMAIN; 1.
 DR SEQUENCE 441 AA; 50472 MW; DC98127FEECE34E2 CRC64;

Query Match 17.9%; Score 376.5; DB 13; Length 441;
 Best Local Similarity 30.3%; Pred. No. 9.6e-23;
 Matches 101; Conservative 61; Mismatches 122; Indels 49; Gaps 14;

QY 60 DEESCQVYTKITREKH-----FMCNLLQNSIVSYTRS---TKKLLRNMDQOASLDVL 112
 DB 142 EMEKHTTDLKSTIKDEKQLOVLYAR--ONSITIELEKQVLTATVNNNSVLOKQOHDL--- 196
 QY 113 SNQVNEIMNRVLLLTTEVFRKQLDPRPRVOSHGLDCTD-IKDTIGSVTKTPSGLYI 171
 DB 197 ---METVHNLTIMSTPNSAKK--NFIAREQISPKDCAEAFKSGL-----TTSGLYTLT 246
 QY 172 PEGSSYFPEVCMQDYGSGGWTVIQRIIDTDFORLMCDYLDGFDLGERFWLGKIKIF 231
 DB 247 FPNSSAQEKAKYCDMESNGGWTVLORRDGSYDFHRTWKYKIGFGDPAGEYWLGNFEVS 306
 QY 232 YIVNOKNTSFMLYVALESDDTLAYASVDNFWLEDETFREFKMHIGRYSGNAGDAFRGLK 291
 DB 307 QLTNQR--YVLKILKMEGNEATLYLDQFYLANEEOKYRIHLKGLGTAGKI-----S 359
 QY 292 EDNQAMPEFSTVDVNDGCRPACLVNGOSVKSCHLNKTGMFNECGLANLNGIHH--- 348
 DB 360 SISQPNDFSTKDDADNDKC-----ICKGSOMLT-GGWMFPDAGCPSNLNGWYPLR 408
 QY 349 -FSGKLATGICQWGTWTKNNSPVKIKISVSMKIR 380
 DB 409 QNNKF--NGIKWYV--KSGYSILKATTMIR 437

Search completed: December 16, 2002, 17:35:44
 Job time : 32.254 secs

QY 130 -----VFRKO---LDP-----PFRPVOSHGL----- 148
DB 188 NOSVMTLLEEOCLRFESKQDTHVSPPLVQVPHILPNSOQYTPGLLGGNEIORBGYPR 247
QY 149 DCTDIKDTIGSVYKTP-----SGLYIIHPEGSSYPFEV 181
DB 248 DLMPRPDLATSPKSPFKIPRYTFINEGPFKDCQAKKAGHSVSGIYMIKPEKNSGPMOL 307
QY 182 MCDMDYRGGMWYIQRKIDGIIDFORLWCDYLDGFGDLLGEFMLGKIKFYIYNQNTSEF 241
DB 308 WCNESLDPGGWYIQRKIDGVSVEFFRNMENYKKGFGNIDGEWLGLENITMLSNQDN--Y 365
QY 242 MLYVALESEDDPLAVASYNFMLEDETRFKMLGRYSGNAGAFGLKEDNQNMPSS 301
DB 366 KLIIELEDMSDKRYVAEYSFRLPESEFYRLGLTYGQNAGDSMMW-----HNGKQFT 419
QY 302 TSDVDNDGCRPACLVNGQSVKCSHLNKTGMWFNEGCLANLNGIHFGSKLLA---TGI 358
DB 420 TIDRDKD-----MYAGNCAHFH-KGGMWYNACAHSNLNGVYRGHYSKQDGI 468
QY 359 QWGTWTKNNSPVKIKSVSKIR 380
DB 469 FWAEX--RGGSYSLRAVQMMIK 488

RESULT 2
US-08-960-507-4
; Sequence 4, Application US/08960507
; Patent No. 6057435

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.

TITLE OF INVENTION: Tie Ligands

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/960,507

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Dregler, Ginger R.

REGISTRATION NUMBER: 33,055

REFERENCE/DOCKET NUMBER: P1130P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-3216

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 491 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-960-507-4

Query Match 20.2%; Score 425; DB 3; Length 491;

Best Local Similarity 26.9%; Pred. No. 1.3e-35;

Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

QY 103 DE-QQASLDYL-----SNOVNELANRVLLITTE----- 129
DB 128 SRVTOYLMOLHEIRKRDNSLELSOLENKILNVTTETMKMATRYRELEVKYASLTDLVN 187
QY 130 -----VFRKO---LDP-----PFRPVOSHGL----- 148
DB 188 NOSVMTLLEEOCLRFESKQDTHVSPPLVQVPHILPNSOQYTPGLLGGNEIORBGYPR 247
QY 149 DCTDIKDTIGSVYKTP-----SGLYIIHPEGSSYPFEV 181
DB 248 DLMPRPDLATSPKSPFKIPRYTFINEGPFKDCQAKKAGHSVSGIYMIKPEKNSGPMOL 307
QY 182 MCDMDYRGGMWYIQRKIDGIIDFORLWCDYLDGFGDLLGEFMLGKIKFYIYNQNTSEF 241
DB 308 WCNESLDPGGWYIQRKIDGVSVEFFRNMENYKKGFGNIDGEWLGLENITMLSNQDN--Y 365
QY 242 MLYVALESEDDPLAVASYNFMLEDETRFKMLGRYSGNAGAFGLKEDNQNMPSS 301
DB 366 KLIIELEDMSDKRYVAEYSFRLPESEFYRLGLTYGQNAGDSMMW-----HNGKQFT 419
QY 302 TSDVDNDGCRPACLVNGQSVKCSHLNKTGMWFNEGCLANLNGIHFGSKLLA---TGI 358
DB 420 TIDRDKD-----MYAGNCAHFH-KGGMWYNACAHSNLNGVYRGHYSKQDGI 468
QY 359 QWGTWTKNNSPVKIKSVSKIR 380
DB 469 FWAEX--RGGSYSLRAVQMMIK 488

RESULT 3
US-09-136-828-4
; Sequence 4, Application US/09136828
; Patent No. 6350450

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.

TITLE OF INVENTION: Tie Ligands

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/136,828

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Dregler, Ginger R.

REGISTRATION NUMBER: 33,055

REFERENCE/DOCKET NUMBER: P1130R1A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-3216

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 491 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-09-136-828-4

Query Match 20.2%; Score 425; DB 4; Length 491;

Best Local Similarity 26.9%; Pred. No. 1.3e-35;

Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

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Db      68  TKGQDASTIKDMITRMDELNKLADYLSROKREIDVQLVVDGNIYEVKLLRKESHNM 127
Qy      103 DE-QQASLDYL-----SNOVNEIMNRVLLLTTE-----129
Db      128 SRVQLYMLLHETIRKRONSLLELSQLENKILNVTTEMLKATRYRELKVKASLIDLVN 167
Qy      130 -----VFRKO---LDP-----PFRPVOSHGL-----148
Db      188 NOSVMITLLEEQCLRIEFSRQDTHVSPLVQVVPQHIFPNSQQYTPGLLGNEIORDPGYPR 247
Qy      149 DCDIDIKDTIGSVTKTP-----SGLYIHPEGSSYTFEV 181
Db      248 DLMPPPLATSPKSPKIPPVTFINEGPPKDCQQAKEAGHSVSGIYMIKRPENSNGMOL 307
Qy      182 MCDMDYRGGWTVYQKRIDGIIDFORLMCDYLDGFDLGEFNLGKIKIFYVNOKNTSF 241
Db      308 WCNSLDPGCVTVYQKRIDSQVNFRRMWNKKGFGNIDGFTWLGLENITMLSNQDN--Y 365
Qy      242 MLVYALSEDDTLAYASYDNFWLEDETRFFKMLGRYSNAGDAFRGLKREDNONAMPFS 301
Db      366 KLIELEDMDSKRYAYEYSSFRLEPESEFYRLRLGTGYQGNAGDSMMV-----HNGKQFT 419
Qy      302 TSDVDNDGCRPACLVNGOSVKSCHLNKTGWMEGCLANLNGIHFGSKLLA---TGI 358
Db      420 TLDKDKD-----MYAGNCAHFH-KGGMWYNACAHSLNGLVWYRGHYRSKHODGI 468
Qy      359 QMGWTWKNNSPVKIKSYMKIR 380
Db      469 FMAEY--RGGSYSILRAVQMMIK 488

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RESULT 4
US-09-332-928A-4
Sequence 4, Application US/09332928A
Patent No. 6368853
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/332,928A
FILING DATE: 14-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/933,821
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-332-928A-4
Query Match 20.2%; Score 425; DB 4; Length 491;
Best Local Similarity 26.9%; Pred. No. 1,3e-35;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

```

Qy      44  SNKDESKNDYCKECCESCQVYKTYTR-EKHFPCRLNLSIVSYSTSKLLRNMM 102
Db      68  TKGQDASTIKDMITRMDELNKLADYLSROKREIDVQLVVDGNIYEVKLLRKESHNM 127
Qy      103 DE-QQASLDYL-----SNOVNEIMNRVLLLTTE-----129
Db      128 SRVQLYMLLHETIRKRONSLLELSQLENKILNVTTEMLKATRYRELKVKASLIDLVN 167
Qy      130 -----VFRKO---LDP-----PFRPVOSHGL-----148
Db      188 NOSVMITLLEEQCLRIEFSRQDTHVSPLVQVVPQHIFPNSQQYTPGLLGNEIORDPGYPR 247
Qy      149 DCDIDIKDTIGSVTKTP-----SGLYIHPEGSSYTFEV 181
Db      248 DLMPPPLATSPKSPKIPPVTFINEGPPKDCQQAKEAGHSVSGIYMIKRPENSNGMOL 307
Qy      182 MCDMDYRGGWTVYQKRIDGIIDFORLMCDYLDGFDLGEFNLGKIKIFYVNOKNTSF 241
Db      308 WCNSLDPGCVTVYQKRIDSQVNFRRMWNKKGFGNIDGFTWLGLENITMLSNQDN--Y 365
Qy      242 MLVYALSEDDTLAYASYDNFWLEDETRFFKMLGRYSNAGDAFRGLKREDNONAMPFS 301
Db      366 KLIELEDMDSKRYAYEYSSFRLEPESEFYRLRLGTGYQGNAGDSMMV-----HNGKQFT 419
Qy      302 TSDVDNDGCRPACLVNGOSVKSCHLNKTGWMEGCLANLNGIHFGSKLLA---TGI 358
Db      420 TLDKDKD-----MYAGNCAHFH-KGGMWYNACAHSLNGLVWYRGHYRSKHODGI 468
Qy      359 QMGWTWKNNSPVKIKSYMKIR 380
Db      469 FMAEY--RGGSYSILRAVQMMIK 488

```

RESULT 5
US-09-136-801-4
Sequence 4, Application US/09136801
Patent No. 6413770
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
Hillan, Kenneth
APPLICANT: Botstein, David
APPLICANT: Goddard, Audrey
APPLICANT: Roy, Margaret
APPLICANT: Ferrara, Napoleone
APPLICANT: Tumas, Daniel
APPLICANT: Schwall, Ralph
TITLE OF INVENTION: Tie Ligand Homologues
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,801
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.

```

;
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-136-801-4

Query Match      20.2%; Score 425; DB 4; Length 491;
Best Local Similarity 26.9%; Pred. No. 1.3e-35;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

QY 44 SNAKDESKNDTVCKEDCESCDVTKITRE-EKHFMCRNLNSIVSYRSTKLLRNMA 102
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
DB 68 TKGQDASTIKDMITRMDELNLKDVLSRQKREIDVQLVVDVGNIVNEVKLLRKSRMNN 127
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
QY 103 DE-QQASLDYL-----SNQVELMNRVLLTTE----- 129
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
DB 128 SRVTQLYQMLHEIIRKRDNSLELSOLENKLINVTTEMLKMATRYRELEVKYASILDVYN 187
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
QY 130 -----VFRKQ---LDP-----FPHRPVQSHGL----- 148
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
DB 188 NOSVMTLLEEOCLRIEFSKQDTHVSPRLVQVYVPHIIPNSQYTPGLLGGNEIQRDPGYR 247
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
QY 149 DCTDIKIDTIGSVTKTP-----SGLYIHPRGSSYPFEV 181
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
DB 248 DLMPRPDLATSTPKSPFKIPRYTFINEGPFKDCQQAKEAGHSVSGIYMKRPNSGPMQL 307
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
QY 182 MCDMDYRGCGWTVIOKRIDGIDFORLMCDYDGFGLDGEFGLGKIKFYIVNOKNTSF 241
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
DB 308 WCENSLDPGCGWTVIOKRIDGVSINFRNMENYKKGFGNIDGEYWLGIENIYMLSNODN--Y 365
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
QY 242 MLYVALESEDDTLAASYDNFWLEDETRFEKMHILGRYSGNAGDARGLKEKNONAMPSS 301
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
DB 366 KLLIELEWMSDKKYAEVSSFRLEPESEFYRLGLTYQGNAQDSMMW-----HNGKQFT 419
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
QY 302 TSDVDNDGCRPACLVNGQSVKCSHLHNKTMGMWNECGLANGLIHHSFGKLLA--TGI 358
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
DB 420 TLDRLDKD-----MYAGNCAPH--KGGWYINACAHSNLNGWYRGGHTRSKHQDCI 468
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
QY 359 QMGWTKNNSPVKIKSVSMKIR 380
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
DB 469 FWAEEY--RGGSYSLRVQVMIR 488
; : | | : | | : | | : | | : | | : | | : | | : | | : | |

RESULT 6
US-09-332-929-4
; Sequence 4, Application US/09332929
; Patent No. 6420542
; GENERAL INFORMATION:
; APPLICANT: Godowskt, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/332,929
; FILING DATE:

```

```

;
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/933,821
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-332-929-4

Query Match      20.2%; Score 425; DB 4; Length 491;
Best Local Similarity 26.9%; Pred. No. 1.3e-35;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

QY 44 SNAKDESKNDTVCKEDCESCDVTKITRE-EKHFMCRNLNSIVSYRSTKLLRNMA 102
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
DB 68 TKGQDASTIKDMITRMDELNLKDVLSRQKREIDVQLVVDVGNIVNEVKLLRKSRMNN 127
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
QY 103 DE-QQASLDYL-----SNQVELMNRVLLTTE----- 129
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
DB 128 SRVTQLYQMLHEIIRKRDNSLELSOLENKLINVTTEMLKMATRYRELEVKYASILDVYN 187
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
QY 130 -----VFRKQ---LDP-----FPHRPVQSHGL----- 148
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
DB 188 NOSVMTLLEEOCLRIEFSKQDTHVSPRLVQVYVPHIIPNSQYTPGLLGGNEIQRDPGYR 247
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
QY 149 DCTDIKIDTIGSVTKTP-----SGLYIHPRGSSYPFEV 181
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
DB 248 DLMPRPDLATSTPKSPFKIPRYTFINEGPFKDCQQAKEAGHSVSGIYMKRPNSGPMQL 307
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
QY 182 MCDMDYRGCGWTVIOKRIDGIDFORLMCDYDGFGLDGEFGLGKIKFYIVNOKNTSF 241
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
DB 308 WCENSLDPGCGWTVIOKRIDGVSINFRNMENYKKGFGNIDGEYWLGIENIYMLSNODN--Y 365
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
QY 242 MLYVALESEDDTLAASYDNFWLEDETRFEKMHILGRYSGNAGDARGLKEKNONAMPSS 301
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
DB 366 KLLIELEWMSDKKYAEVSSFRLEPESEFYRLGLTYQGNAQDSMMW-----HNGKQFT 419
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
QY 302 TSDVDNDGCRPACLVNGQSVKCSHLHNKTMGMWNECGLANGLIHHSFGKLLA--TGI 358
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
DB 420 TLDRLDKD-----MYAGNCAPH--KGGWYINACAHSNLNGWYRGGHTRSKHQDCI 468
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
QY 359 QMGWTKNNSPVKIKSVSMKIR 380
; : | | : | | : | | : | | : | | : | | : | | : | | : | |
DB 469 FWAEEY--RGGSYSLRVQVMIR 488
; : | | : | | : | | : | | : | | : | | : | | : | | : | |

RESULT 7
US-09-442-143A-2
; Sequence 2, Application US/09442143A
; Patent No. 6403089
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; APPLICANT: Clark, David A.
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-14
; CURRENT APPLICATION NUMBER: US/09/442,143A
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 60/046,537
; PRIOR FILING DATE: 1997-05-17
; PRIOR APPLICATION NUMBER: US 60/061,684
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2

```


LENGTH: 439
TYPE: PRF
ORGANISM: Homo sapiens fg12
US-09-442-143A-2

Query Match 19.7%; Score 413.5; DB 4; Length 439;
Best Local Similarity 30.2%; Pred. No. 1.7e-34;
Matches 119; Conservative 61; Mismatches 147; Indels 67; Gaps 15;

QY 34 SSVNIVEDGSNAKDESKSDTYCKEDCE-----ESCQVTKT 70
DB 73 SRIEVEKQVONLKEIYNSLKKSC-QDCKLOADNGDPGRGLLPSTGAPGEVDNRVR 131
QY 71 ITREKHEKCRNLONS-----IVSYTRSTKRLRNM-----MDEQASLDYLSNQVHELM 120
DB 132 ELSEVYKLSSELKNAKEEINVLHGRLKELNLYMNNIENYVDSKANLFFVNSLDGKC 191
QY 121 NRVLITTEFRKQLODFPHRPQVSHL--DCTDIKDTIGSVYKTPSGLYIHPGSSYP 178
DB 192 SKC-----PSQEQIOSRPVQ-HLIYKDCSDY---AIGRSSEYRVPDPKNS 237
QY 179 FEVACDMHYGGGWTVIQRKIDGIIDFQRLMCDYLDGFDLLGEFWMGLKKIYIVQKN 238
DB 238 FEVYCMETGCGWTVIQAARLDGSTNTRWQDYKAGFGLRREFWLGNDKIHLLT--KS 295
QY 239 TSFMYALLESDDTLAYASYDNFMLEDETRFEKMLGRYSNGADAFRLKKEDNONAM 298
DB 296 KEMILRIDLEDNGVELYALYDQFYVANEFLKRYLHVGNVNGTGDALR-FNKHYNDLK 354
QY 299 PFSISDVNDGCRACILYVNSQSVKSHLANKTGWMFNEGLANLNG-IHFFSGKLATG 357
DB 355 FETTPDKDNDRYPBG-----NCG-LYSSGWMFDCIASLANLNGKYYHQKRYGVANG 404
QY 358 IONGTW--TKNSPVKIKSYSMKIRMYNP-YFK 388
DB 405 IFWGTWPGVSEARHPGKYSSEKKAAMIRKHKR 438

RESULT 8
US-09-442-143A-4
Sequence 4, Application US/09442143A
Patent No. 6403089
GENERAL INFORMATION:
APPLICANT: Levy, Gary
APPLICANT: Clark, David A.
TITLE OF INVENTION: Methods of Modulating Immune Coagulation
FILE REFERENCE: 9579-14
CURRENT APPLICATION NUMBER: US/09/442,143A
CURRENT FILING DATE: 1999-11-15
PRIOR APPLICATION NUMBER: US 60/046,537
PRIOR FILING DATE: 1997-05-17
PRIOR APPLICATION NUMBER: US 60/061,684
PRIOR FILING DATE: 1997-10-10
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 432
TYPE: PRF
ORGANISM: Murine fg12
US-09-442-143A-4

Query Match 19.3%; Score 405.5; DB 4; Length 432;
Best Local Similarity 35.4%; Pred. No. 1.1e-33;
Matches 110; Conservative 43; Mismatches 115; Indels 43; Gaps 13;

QY 98 LRNMMDQQA-----SIDYLSNOVNEMLNRVLITTEFRKOLD-----PFP 139
DB 137 LKNAKDDIOIGQLRLETLHLVNMNNIENYVDSKANLFFVNSLDGKSCPSOEHMQ 194
QY 140 HRPQSHGL--DCTDIDTIGSVYKTPSGLYIHPGSSYPFEVYCMETGCGWTVIQR 197
DB 195 SQPVQ-HLIYKDCSD-HYVIG---RSSGAYRVPDPKNSFEVYCMETGCGWTVIQA 249

QY 198 RIDGIIDFQRLMCDYLDGFDLLGEFWMGLKKIYIVQKNKTSFMYALLESDDTLAYA 257
DB 250 RLDGSTNTRWQDYKAGFGLRREFWLGNDKIHLLT--KSKEMILRIDLEDNGFGLTFLYA 307
QY 258 SYDNFMLEDETRFEKMLGRYSNGADAFRLKKEDNONAMPESTSDVNDGCRACILYN 317
DB 308 LYDQFYVANEFLKRYLHVGNVNGTGDALR-FSRHYNDLREFFTYPRDNDRYPBG---- 362
QY 318 GQSVKCSHLNKGWMFNEGLANLNG-IHFFSGKLATGIONGTWTKN--SPVKRS 374
DB 363 -----NCG-LYSSGWMFDCIASLANLNGKYYHQKRYGVANGIFWGTWPGVSEARHPGKYS 416
QY 375 VSMKIRMYNP 385
DB 417 SFOAKMMIRP 427

RESULT 9
US-08-740-223A-12
Sequence 12, Application US/08740223A
Patent No. 6265564
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: Expressed ligand - vascular
TITLE OF INVENTION: Intercellular Signalling Molecule
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill Road
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/740,223A
FILING DATE: 25-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 60/022/999
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Cobert, Robert J
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 333
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEFAX: 914-345-7721
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 490 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: hTLL1
LOCATION: 1...490
OTHER INFORMATION: human TIE-2 ligand 1
US-08-740-223A-12

Query Match 19.3%; Score 405.5; DB 4; Length 490;
Best Local Similarity 27.5%; Pred. No. 1.4e-33;
Matches 118; Conservative 65; Mismatches 125; Indels 121; Gaps 16;

QY 23 VQGCYVHSHDSSVYVIVEDGSNAKDESKSDTYCKEDCESCVYKIRIREEHFKCRN 82
DB 108 IQQNAVONHT---ATMLEIGTSLISDT-----AQTRKLTVDVETQVNLQTSRLEIQL 156


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OY 103 DEQASLDYLSNOV-----ELM-----NRVLLTTEVF-----RKQIDFP 139
Db 224 TRQTYIQLELEKOLNATTNNSVLOKQOLEMDTQVHNLVNLCTKEVLLKGGKREBEKPF- 282
OY 140 HRPVQSHGLDCTDIKFTIGSVTKTPSGLYIHPBGSSYPRVWCDMDYRGGMVYIQRI 199
Db 283 -----RDCADVY-----QAGFNKSGIYTYIYNMBPKVFCNMVDVNGGWTYIQHRE 330
OY 200 DGIIDFORLWCYUJLDGFGDILGEFGLGKTFYIVNOKNTSEFMYLYVALESDDTLAVASY 259
Db 331 DQSLDPQRQMKKEKMGFGNPSGEYWLGNETFAITTSQR--QYMLRIELMDEGNRAVSQY 388
OY 260 DNFWEDETRFRKMLGRYSQGNAGDAFRGLKEDN--ONAMPFSTSDVNDGCRPAC--L 315
Db 389 DRFHIGNEKQVRYLTKHGHTAG-----KQSSLHGHGDEFSTKROADNDNCMKCALM 441
OY 316 VNGQSVKSCSHLHNTKGWMEFNECCGLANLNGIHHSQ---KLATGCIOMGTWTKNNSPVK 371
Db 442 LUG-----GWMFDACGSPMLNMGMYTAGONHRKL--NGIKWHYF--KGPSYS 484
OY 372 IKSYSMKIR 380
Db 485 LRSTJTMIR 493

```

```

RESULT 12
US-09-709-188-4
; Sequence 4, Application US/09709188
; Patent No. 6441137
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
; FILE REFERENCE: REG 333-2
; CURRENT APPLICATION NUMBER: US/09/709,188
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-709-188-4

Query Match          19.2%; Score 403.5; DB 4; Length 497;
Best Local Similarity 27.3%; Pred. No.2.3e-33;
Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

QY 23 VQNCVHSTSSVNIIVEDGNSNAKDESKSNDYCKDECESDVKRTITREEKHFMQRN 82
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 115 IQQNAVQNHHT---ATMLEIGTSLISQT-----AQTRKRLDVENQVNLQTSRLQIQL 163
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 83 LQNSIVSY-----TRSTKILRRMM 102
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 164 LENSISTYKLEKQLLOQTNEILKIHKRNLSLEHKILEMEGKHKELDTLKKEKKNLQGLV 223
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 103 DEQOASLDYLSQNV-----ELM---NRVLLLTTEVF-----RKOLDPEP 139
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 224 TRQTYIIOELEKQNLBATNNSVLOKQOQLELMQVHNLVNLCTREVLILKGKREERKF- 282
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 140 HRPVQSHGLDCDIDIKRTIGSVYTKPSGLYIIHPGSSYPREVQCDMDYRGGGMYIQKRI 199
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 283 -----RDCADVY-----QAGFNKSSGIYIYINNMPEPKVFPCNMVNVGGGWYIOHRE 330
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 200 DLIIDFQRLMCDYLDLDFGDLDFEFGDLGLKRTFYIVNQKNTSFMLYVALSEDDFLAYASY 259
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 331 DCSLDPRQRGKMKKEYKMGFGNPSGEYVLGNIEFIATISOR--QYMRILEMDWEGNRATYSQY 388
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 260 DNFWLEDETRFEKMHKGRYSGNAGDAFRGLAKEDN--QNMPESTSDVNDGCRPAC--L 315
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 389 DFFHIGNEQNRYRLYLKGHGHTAG-----KSSLILHGADEFSTKADNDNMCCKCALM 441
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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[illegible]

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1      RESULT 13
2      US-08-373-579-4
3      ; Sequence 4, Application US/08373579
4      ; Patent No. 5650490
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Davis, et al.
7      ; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
8      ; TITLE OF INVENTION: THEREOF
9      ; NUMBER OF SEQUENCES: 6
10     ; CORRESPONDENCE ADDRESS:
11     ; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
12     ; STREET: 777 Old Saw Mill River Road
13     ; CITY: Tarrytown
14     ; STATE: New York
15     ; COUNTRY: USA
16     ; ZIP: 10591
17     ;
18     ; COMPUTER READABLE FORM:
19     ; MEDIUM TYPE: Floppy disk
20     ; COMPUTER: IBM PC compatible
21     ; OPERATING SYSTEM: PC-DOS/MS-DOS
22     ; SOFTWARE: PatentIn Release #1.0, Version #1.30
23     ; CURRENT APPLICATION DATA:
24     ; APPLICATION NUMBER: US/08/373,579
25     ; FILING DATE: 17-JAN-1995
26     ; CLASSIFICATION: 435
27     ;
28     ; PRIOR APPLICATION DATA:
29     ; APPLICATION NUMBER: US 08/353,503
30     ; FILING DATE: 09-DEC-1994
31     ; PRIOR APPLICATION DATA:
32     ; APPLICATION NUMBER: US 08/348,492
33     ; FILING DATE: 02-DEC-1994
34     ; PRIOR APPLICATION DATA:
35     ; APPLICATION NUMBER: US 08/330,261
36     ; FILING DATE: 27-OCT-1994
37     ; PRIOR APPLICATION DATA:
38     ; APPLICATION NUMBER: US 08/319,932
39     ; FILING DATE: 07-OCT-1994
40     ; ATTORNEY/AGENT INFORMATION:
41     ; NAME: CoBERT, Robert J.
42     ; REGISTRATION NUMBER: 36,108
43     ; REFERENCE/DOCKET NUMBER: REG 330-D
44     ; TELECOMMUNICATION INFORMATION:
45     ; TELEPHONE: (914) 345-7400
46     ; TELEFAX: (914) 345-7721
47     ; INFORMATION FOR SEQ ID NO: 4:
48     ; SEQUENCE CHARACTERISTICS:
49     ; LENGTH: 497 amino acids
50     ; TYPE: amino acid
51     ; TOPOLOGY: linear
52     ;
53     ; MOLECULE TYPE: protein
54     ;
55     ; US-08-373-579-4
56
57     Query Match      19.1%; Score 402.5; DB 1; Length 497;
58     Best Local Similarity 27.3%; Pred.No.2,9e-33;
59     Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;
60
61     QY 23 VQGNICVHSTSDVYVNIYEDGSSNADDEKSSNDYCKEDCEESCDYKTKITREKHFMCN 82
62     DB 115 IQGNVQVNIHT--ATMLEIGTSLSQT-----AEQTRKLIDVETQVLANQTSKLEIQL 163
63     QY 83 LQNSTVSY-----TRSTRKLLIRNM 102
64     1-111-:1
65     164 IENSLSTYLEKQLQQTNEILKIEKNLSLLEKILLEMGRKRELDITLKEKENIGLY 223

```

QY 103 DEQASDIYLSNVN-----ELM-----NRVLLITTEVF-----RKOLDPPP 139
DB 224 TRQTYIIQELERKQLRATNTNSVLQKQOLELMDIVNLVNLCTKRVLLKGGKREEDKPF- 282
QY 140 HRPVSHGLDCTDIKDTIGSVTKTPSPGLYIIHPGSSYPFEVYMDYRGGMVYIQR 199
DB 283 -----RDCADY-----QAGFNKSGIYIIYINNMPPEKKVFCMADVNGGWTYIQHRE 330
QY 200 DGIIDFORLWCDYLDGFDLLGEFWLGLKIFYIVNQKNTSPMLVVALESEDDTLAVASY 259
DB 331 DGSIDFQGMKREYKMGFGNPSGEYWLGNFIFATISQR--QYMLRIELMDMGNRAYSQY 388
QY 260 DNFWEDETRFFKMLLGRKXSGNAGDAFRGLKEDN--QNAPEFSISDVNDGCRPAC--L 315
DB 389 DRFHGNKQNYRLYLKHTGTAG-----KQSLILHGADEFSTKADNDNCMCCKALM 441
QY 316 VNGQSVKSCSHLHNTGWMFNECGLANINGIHFS---GKLLATGIOMGTWTKNNSPVK 371
DB 442 LTG-----GWMFDACGPSNLGMFYTAGQNHGKL--NGIKWHYF--KGPSYS 484
QY 372 IKSVSMKIR 380
DB 485 LRSTTMIR 493
RESULT 14
US-08-418-595-4
Sequence 4, Application US/08418595
Patent No. 5814464
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,595
FILING DATE: 06-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,579
FILING DATE: 17-JAN-1995
APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Cobert, Robert J.
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-418-595-4
Query Match 19.1%; Score 402.5; DB 2; Length 497;
Best Local Similarity 27.3%; Pred. No. 2.9e-33;
Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;
QY 23 VQGNVHNHSTDSVYNIYEDGSNADESKSNDTVCEKECEESCDYKTRITREKHFMRN 82
DB 115 IQQNAVQNT-----ATMLEIGTSLST-----ABQTRKLTVETVYLNQTSRLTIQL 163
QY 83 LQNSIVS-----TRSTKLLRNM 102
DB 164 LENSISTYKLEKQLQOTNEILKIEKNSLLEHKILEMGKHEBDLTLKEKENLQGLV 223
QY 103 DEQASDIYLSNVN-----ELM-----NRVLLITTEVF-----RKOLDPPP 139
DB 224 TRQTYIIQELERKQLRATNTNSVLQKQOLELMDIVNLVNLCTKRVLLKGGKREEDKPF- 282
QY 140 HRPVSHGLDCTDIKDTIGSVTKTPSPGLYIIHPGSSYPFEVYMDYRGGMVYIQR 199
DB 283 -----RDCADY-----QAGFNKSGIYIIYINNMPPEKKVFCMADVNGGWTYIQHRE 330
QY 200 DGIIDFORLWCDYLDGFDLLGEFWLGLKIFYIVNQKNTSPMLVVALESEDDTLAVASY 259
DB 331 DGSIDFQGMKREYKMGFGNPSGEYWLGNFIFATISQR--QYMLRIELMDMGNRAYSQY 388
QY 260 DNFWEDETRFFKMLLGRKXSGNAGDAFRGLKEDN--QNAPEFSISDVNDGCRPAC--L 315
DB 389 DRFHGNKQNYRLYLKHTGTAG-----KQSLILHGADEFSTKADNDNCMCCKALM 441
QY 316 VNGQSVKSCSHLHNTGWMFNECGLANINGIHFS---GKLLATGIOMGTWTKNNSPVK 371
DB 442 LTG-----GWMFDACGPSNLGMFYTAGQNHGKL--NGIKWHYF--KGPSYS 484
QY 372 IKSVSMKIR 380
DB 485 LRSTTMIR 493
RESULT 15
US-08-665-926-4
Sequence 4, Application US/08665926
Patent No. 5851797
GENERAL INFORMATION:
APPLICANT: Valenzuela et al.
TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,926
FILING DATE: 19-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robert J. Cobert
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-H

TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-2113
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-665-926-4

Query Match 19.1%; Score 402.5; DB 2; Length 497;
Best Local Similarity 27.3%; Pred. No. 2.9e-33;

Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

QY 23 VQNCVHSTDSVNVNVEDSGSNKDESKSNDYCKEDCECDVCKTKITREKHFMCRN 82
Db 115 IQNNAVQNHNT---ATMLETSTLSLT-----AEQTRKLTDETVQLNQTSLRYQL 163
QY 83 LQNSIVSY-----TRSTKLLRNMM 102
Db 164 LENSLSYTKLEKQLQQTNEILKHEKNSLLEHKLLEMEGKHKELDTLKEKENLQGLY 223
QY 103 DEQASLDYLSNOVN-----ELM-----NRVLLTTEVF-----RKQLDPP 139
Db 224 TRQTYIIQELKEKQLNRATTNNSVLQKQOLELMDYVHNLVNLCTKEVLLKGGKREEDKPF- 282
QY 140 HRPVQSHGLDCTDIKDTIGSVTKTPSGLYIHPGSSYPRFVCMGDMOYRGSGWTYIOKRI 199
Db 283 -----RDCADYV-----QAGFNKSGITYITYINNMEPKRVFCNMVDVGGGWTVIQHRE 330
QY 200 DGIIDFQRLMCDYLDGFGDLGEPFLGLKIFYIVNOKNTSFMLYVALESEDDTLAVASY 259
Db 331 DGSIDFQRGWKEYMGFGNPGSEYWGNEFIFATLSQR--QYMLRIELMDWEGNRAYSQY 388
QY 260 DNFLEDETRFFKMHGLGYSNAGDAFRGLKEDN--ONAMPFSTSDVNDGCRPAC--L 315
Db 389 DRFHIGNEKQYRLYLGHGTGTAG-----KOSSLILHGADFSTKDADNDNCMKCALM 441
QY 316 VNGSVKSCSHLHNKGTGWFNECGLANLNGIHHS---GKLLATGIQMGTWTKNNSPVK 371
Db 442 LTG-----GHWFDACGSPNLNGMFTAGQNHGKL--NGIKWHYF--KGPSYS 484
QY 372 IKSVSMKIR 380
Db 485 LRSTTMIR 493

Search completed: December 16, 2002, 17:36:52
Job time: 14.3175 secs

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OM protein - protein search, using sw model

Run on: December 16, 2002, 17:32:58 ; Search time 14.6032 Seconds
(without alignments)
2422.587 Million cell updates/sec

Title: US-09-596-196-9

Perfect score: 2000

Sequence: 1 EVYQGNCHVHSTDSYVNTV.....PVKIKSVSMKIRRMNPFYK 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	413.5	20.7	439	2 I37391	fibritogen-like pr
2	405.5	20.3	432	2 A27447	cytotoxic T-lympho
3	401.5	20.1	432	2 I56934	fibritogen-like pr
4	397	19.9	312	2 JN0596	fibritogen-like pr
5	394.5	19.7	468	1 FGB0B	fibritogen beta ch
6	375.5	18.8	491	1 FGHUB	fibritogen beta ch
7	371.5	18.6	437	1 FGHUG	fibritogen beta ch
8	371.5	18.6	453	1 FGHUGB	fibritogen beta ch
9	371.5	18.6	463	1 A38463	fibritogen beta ch
10	370	18.5	479	2 A25052	fibritogen beta ch
11	365	18.2	444	2 S05313	fibritogen gamma-B
12	360	18.0	432	2 FGLMGS	fibritogen gamma-B
13	352.5	17.6	438	2 A32670	fibritogen gamma c
14	350.5	17.5	282	2 A35084	fibritogen gamma c
15	348.5	17.4	774	2 A39832	fibritogen-related
16	346.5	17.3	328	2 A05299	scabrous locus (sc
17	337.5	16.9	866	2 D44234	fibritogen beta ch
18	330	16.5	1356	2 A45445	fibritogen alpha c
19	329	16.4	334	2 JC5540	januin precursor,
20	328.5	16.4	641	1 A41932	fibritogen precursor
21	327.5	16.4	1353	1 JH0675	fibritogen alpha-I
22	312	15.6	323	2 A47172	restictin precurs
23	311.5	15.6	457	1 FGRGTB	transferrin growth
24	311.5	15.6	445	1 FGRGTB	fibritogen gamma-A
25	311	15.6	4135	2 T42629	tenascin-X - bovin
26	310.5	15.5	1810	1 A32230	tenascin precursor
27	304.5	15.2	1914	2 T42635	tenascin X precurs
28	303.5	15.2	326	2 S61517	tenascin-X precurs
29	302.5	15.1	356	1 A40701	tenascin-X precurs

30	299	14.9	417	2 S65944	tenascin-X - pig (
31	296	14.8	226	2 S28170	tenascin homolog -
32	295	14.8	320	2 B47172	fibritogen-beta - pig
33	286	14.3	860	2 I48839	tenascin-X - mouse
34	284.5	14.2	2019	1 J01322	tenascin precursor
35	283.5	14.2	4008	2 T09070	probable tenascin
36	282.5	14.1	1746	1 A31964	tenascin precursor
37	271	13.6	2201	2 A32160	tenascin-C - human
38	212.5	10.6	463	2 T15876	hypothetical prote
39	180.5	9.0	915	2 T21773	hypothetical prote
40	180.5	9.0	927	2 T21772	hypothetical prote
41	173	8.6	431	2 T29850	hypothetical prote
42	154.5	7.7	933	2 A31930	cytotactin - chick
43	128.5	6.4	452	2 T26827	hypothetical prote
44	117	5.9	127	2 PC2036	microfibril-associ
45	110.5	5.5	4588	2 T28667	dyein beta heavy

ALIGNMENTS

RESULT 1

I37391
fibritogen-like protein expressed in T lymphocytes (PT49) - human
C:Species: Homo sapiens (man)
C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000
C:Accession: I37391; S47273
R:Ruegg, C.; Pytel, R
Gene 160, 257-262, 1995
A>Title: Sequence of a human transcript expressed in T-lymphocytes and encoding a fib
A:Reference number: I37391; MUID:95369700; PMID:7642106
A:Accession: I37391
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-439 <RES>
A:Cross-references: EMBL:Z26531; NID:9535184; PIDN:CAA85298.1; PID:9535185
A>Note: submitted to the EMBL Data Library, August 1994
C:Superfamily: fibritogen gamma chain; fibritogen beta/gamma homology
F:210-435/Domain: fibritogen beta/gamma homology <PBG>

Query Match	20.7%	Score	413.5;	DB 2;	Length	439;
Best Local Similarity	30.2%	Pred. No.	2.9e-25;			
Matches 119;	Conservative 61;	Mismatches 147;	Indels 67;	Caps 15;		
OY	14	SSVNIYEDGSNAKDESKSNDTVCKEDCE-----ESCQVKT	50			
DB	73	SRIEVEKKEVONLKEIYNLSKKSC-QDCKIQADNDGDPGRNGLLPSTGAPGEVDNKR	131			
OY	51	ITREKEHFMCRNLQNS---IVSYTRSTFKLLRNM-----MDEQASLDYLSNQVELM	100			
DB	132	ELESEVVKLSSELNKAKEIIVLGRLEKLVLMNNIENVDSKVNLTFFVNSLDGKC	191			
OY	101	NRULLITTEVFRKQDPEPPHPVOSHGL--DCTDIKDTIGSVYTPSGLYTIHPGSSYP	158			
DB	192	SKC-----PSQEQIQRVQ-HLIYKDCSDYY---AIGKRSSETYRTPDPNNSS	237			
OY	159	FEVACDDYRGSGWTVIOKRIDGIIDFQRLCVDLDGDLGPFWLGKIFPIVQNK	218			
DB	238	FEVCDMETMGSGWTVIOARLDGSTNFTKWQDKAGFGLRRPEWLGNDIHLIT--KS	295			
OY	219	TSFMLYVALESEDDTLAYASYDNFMLEDETRFFKMLGRYSGNAGDAFRLKKEEDNONAM	278			
DB	296	KEMILRIDLEDGFCVVEIYALDYQYVANEFLKYLRLHGVNVTGADLAR-FNKIYNNDLK	354			
OY	279	PEFSIDVDNDCRACLVNGQSVKSCSLHAKTKTGMWNEGCLAND--IHFFSKLLATG	337			
DB	355	FFTPPDKDNDRYPSG-----NCG-LYYSSQMWPDACLSANLNGKYYHQRYGVANG	404			
OY	338	IOWGFW--TKNNSPVKIKSVSMKIRRMNPFYK	368			
DB	405	IFWGTWPGVSEAHPGGYKSSFEKAKMIRPKHF	438			

RESULT 2

A27447

Cytotoxic T-lymphocyte-specific protein precursor (clone pT43) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence,revision 15-Dec-1988 #text,change 03-Dec-1999

C:Accession: A27447

R:Koyama, T.; Hall, L.R.; Haseg, W.G.; Tonegawa, S.; Saito, H.

Proc. Natl. Acad. Sci. U.S.A. 84, 1609-1613, 1987

A:Title: Structure of a cytotoxic T-lymphocyte-specific gene shows a strong homology to F:203-428/Domain: fibrinogen beta/gamma homology <EBG>

A:Reference number: A27447; MUID:81175527; PMID:3550794

A:Accession: A27447

A:Molecule type: mRNA

A:Residues: 1-432 <KB>

A:Cross-references: M616238; NID:g193304; PIDN:AAA37624.1; PID:g387156

C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology

Query Match 20.3%; Score 405.5; DB 2; Length 432;

Best Local Similarity 35.4%; Pred. No. 1,26-24;

Matches 110; Conservative 43; Mismatches 115; Indels 43; Gaps 13;

Db 78 LRRNMDDEQA-----SDLYLSNQVLELNRRVLLTTEVFRKQD-----PFP 119

137 LKNNAKQIQIGLQGRLETLHLVNNNIENTYVDNKAANLVVV--NSLDKCSKCPSEHMQ 194

120 HRPVQSHGL-DCTDIDKDTISVTKTPSGILYIHPEGSYFEVWCMDYDGGGWTYQK 177

195 SOPVQ-HLIYKDCSD-HYVLG--RRSSGAYRVPRDHRNSSFEVYCDMETGGGWTYQA 249

QY 178 RIDGIIDQRILMCDYLDGFDGLGEFWLGLKKIFIVNOKNTSPFLYVALESDDTLAA 237

Db 250 RLDSGTNTRFMKWDKAEFGNLEREFWLGNDKIHILT--KSEMLIRIDLDPFNGLTLYA 307

QY 238 SYDNFLEDETERFEFMHIGRYSGNAGDAFRGLKKEKDNONAPFSDVDNDCRPACLVN 297

Db 308 LYDQYVANEFLKRYLRLHIGNNGTAGDAR-FSRRIYNHDLFFPTTPDDNDNRYPBG---- 362

QY 298 GQSVKSCSHLHNKGWFMNECGLANLNG-IHHSGLLATGIQWCTWTNKN--SPVKIKS 354

Db 363 -----NCG-LYSSGQWPDSCLSANLNGKYHOKYKGYRNIIFWGTWGINDAOPGGYKS 416

QY 355 VSMKIRRYNP 365

Db 417 SFKQAKMIRP 427

RESULT 3

I56934

fibrinogen-like protein - mouse

C:Species: Mus sp. (mouse)

C:Date: 26-Jul-1996 #sequence,revision 26-Jul-1996 #text,change 03-Dec-1999

C:Accession: I56934

R:Paar, R.L.; Funz, L.; Reneker, J.; Myers-Mason, N.; Lebowitz, J.L.; Levy, G.

J. Virol. 69, 5033-5038, 1995

A:Title: Association of mouse fibrinogen-like protein with murine hepatitis virus-induces

A:Reference number: I56934; MUID:95333285; PMID:7669073

A:Accession: I56934

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-432 <RES>

A:Cross-references: GB:S78773; NID:g1042169; PIDN:AAB3482.1; PID:g1042170

C:Genetics:

A:Gene: musfibp

C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology

F:203-428/Domain: fibrinogen beta/gamma homology <EBG>

Query Match 20.1%; Score 401.5; DB 2; Length 432;

Best Local Similarity 35.0%; Pred. No. 2,66-24;

Matches 109; Conservative 43; Mismatches 116; Indels 43; Gaps 13;

Db 78 LRRNMDDEQA-----SDLYLSNQVLELNRRVLLTTEVFRKQD-----PFP 119

137 LKNNAKQIQIGLQGRLETLHLVNNNIENTYVDNKAANLVVV--NSLDKCSKCPSEHMQ 194

RESULT 4

RGBOB

fibrinogen-related protein HFRP-1 precursor - human
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C:Accession: JN0596
R.Yamamoto, T.; Gotloh, M.; Sasaki, H.; Terada, M.; Kitajima, M.; Hirohashi, S.
Biochem. Biophys. Res. Commun. 193, 681-687, 1993
A>Title: Molecular cloning and initial characterization of a novel fibrinogen-related
A:Reference number: JN0596; MUID:93290661; PMID:8390249
A:Accession: JN0596
A:Molecule type: mRNA
A:Residues: 1-312 <YMM>
A:Cross-references: GB:D14446; NID:g9393314; PIND:BA003336.1; PID:g9393315
A:Experimental source: liver
C:Superfamily: fibrinogen beta/gamma homology
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-312/Product: fibrinogen-related protein HFRP-1 #status predicted <MAT>
F:80-305/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 19.9%; Score 397; DB 2; Length 312;
Best Local Similarity 34.3%, Pred. No. 3.9e-24;
Matches 111; Conservative 44; Mismatches 115; Indels 54; Gaps 12;

QY 67 IVSTVRSFKLLRNMDQASLDYLSNQVNELMNRVLITTEVERKQ----- 114
Dd 4 VFSEFLVTTALI---MGREISALEDCAOEOMRLRAQVRILLETRVMOOVKIKQLDENEV 60
QY 115 --LDFPHIRPVQSHG----LDCTDIKDITTSYVKTPSGGLYIIHPEGSSYPEVCNDY 167
Dd 61 QFLDKGEDDYVDLGSKROYADSCSEIFNDGYKL---SGFYKIKPLQSPAEFSYCDS- 115
QY 168 RGGGTVAIOKRRIIDGIIDROLMCVDLDGFGLD--GEFWGLKKIPIYVOKMTSEMLY 224
Dd 116 DGGCVTVIORSDGSSENRRGMKYENGFNGFVQKHGTYWGNKNLHLTTOED--YLK 173
QY 225 VALESDEDTLAYASYDNFMLEDETRFFRMILGRYSGNAGDAFRGLKEDNO---NMP 279
Dd 174 IDLADFEEKNSRYAQKKNFVKVEYELNIGERYSGTAGNFHREVQMMASSHQMK 233
QY 280 FSTSDVDNDGCRPAICLVGVGQSKCSHLHNKTGWMFNECGLANLINGIHESGKLLA---T 336
Dd 234 FSTYDRDHNDNEGCAEDQS-----GWMFNCHSANLNGV-YSGPYTAKTDN 281
QY 337 GIOWGTWTNNSPVAKIKSVSMKIR 360
Dd 282 GIWVITW--HGMYISLKSVYAKIR 303


```

fibrinogen beta-chain - bovine
N:Contains: fibrinopeptide B
C:Species: Bos primigenius taurus (cattle)
C:Date: 29-Jul-1991 #sequence,revision 29-Jul-1991 #text-change 13-Sep-1996
C:Accession: A03122; B03117; B37507; A37513; S02443
R:Blomback, B.; Doolittle, R.F.
Acta Chem. Scand. 17, 1816-1819, 1963
A:Title: The sequence of amino acids at the N-terminal end of bovine fibrinopeptide B.
A:Reference number: A03122
A:Accession: A03122
A:Molecule type: Protein
A:Residues: 1-4 <BL0>
R:Sjogquist, J.; Blomback, B.; Wallen, P.
Ark. Kent 16, 425-436, 1960
A:Title: Amino acid sequence of bovine fibrinopeptides.
A:Reference number: A03117
A:Accession: B03117
A:Molecule type: Protein
A:Residues: 5-21 <SJO>
R:Matthielli, R.A.; Inglis, A.S.; Rubira, M.R.; Hageman, T.C.; Hurrell, J.G.R.; Leach, S.
Arch. Biochem. Biophys. 192, 27-32, 1979
A:Title: Amino acid sequences of portions of the alpha and beta chains of bovine fibrinogen.
A:Reference number: A37507; MUID:79164394; PMID:434821
A:Accession: B37507
A:Molecule type: protein
A:Residues: 22-53 <MAR>
R:Chung, D.W.; Rixon, M.W.; MacGillivray, R.T.A.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 78, 1466-1470, 1981
A:Title: Characterization of a cDNA clone coding for the beta chain of bovine fibrinogen.
A:Reference number: A37513; MUID:81199477; PMID:6262803
A:Accession: A37513
A:Molecule type: mRNA
A:Residues: 44-468 <CHU>
R:Medved, L.V.; Platonova, T.N.; Litvinovich, S.V.; Lukinova, N.I.
FEBS Lett. 232, 56-60, 1988
A:Title: The cleavage of beta-chain in bovine fibrinogen D(H) fragment (95 kDa) leads to
A:Reference number: S02443; MUID:86211875; PMID:2966748
A:Accession: S02443
A:Molecule type: Protein
A:Residues: 373-374 <MED>
C:Comment: Thrombin cleaves the bond between Arg-21 and Gly-22 to release fibrinopeptide
C:Comment: Fibrinogen is a hexamer containing two sets of three nonidentical chains (alpha
C:Keywords: blood coagulation; glycoprotein; plasmin; pyroglyutamic acid; sulfoprotein
E:7-6-205/Domain: fibrinogen disulfide ring homology <FDR>
E:215-464/Domain: fibrinogen beta/gamma homology <BGC>
E:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
E:6/Binding site: sulfate (Tyr) (covalent) #status experimental
E:21-22/Cleavage site: Arg-gly (thrombin) #status experimental
E:371/Binding site: carboxylate (Asn) (covalent) #status predicted
E:372-373/Cleavage site: Arg-Thr (plasmin) #status experimental

Query Match          19.7%: Score 394.5; DB 1; Length 468;
Best Local Similarity 27.5%: Pred. No. 1e-23;
Matches 120; Conservative 54; Mismatches 145; Indels 117; Gaps 16;

QY 7 CVNHSIDSSVNIYEDGSNAKDESKNDYVCKEDEESCDVTKTKTIREKHF--MCRNIQ 64
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 72 CLHADPDLGVL-----|-----CPGCKGLQDTLYRBERPRKRSIEDLR 108
                                     |
QY 65 NSIYTYSTYK-----LLRNMDQOASLDYLSNOVNEIMN-----101
   |::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 109 NTVDVSSTSSSTQFYITLLKNMWMKRONOVODNENNVNNEVSHLEKHQLYIDTVKNNI 168
                                     |
QY 102 -----RVLLITTFVFRKQIDPP-----HRPQSHGLDCTDIDKDTIGS 139
   || | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 169 PTKLVNLSIENLNSKIQKLESADVSTOMEYCRPPCTVTCNIPVVS--GKECEKIIRNGE 227
                                     |
QY 140 VTKPFGSLYIIIEGSSPYFEVCMDDYRGGMVYQIRIGIIDFORLACMDYLDGFDL 199
   |::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 228 T-----SEMTLLQPEDESSKPYRNYCDMKTEKGWYIYQKROGOSLDGFKMNPYKQGFNTI 283
                                     |
QY 200 L-----GEFWLGLKKFIYINQKNTSEMLYVALESEDDTLVASYDNFMWLEDE 247

```

Db | | | | | : | : | : | : | : | : | : | : | : | : | :
284 ATNAGKRYCQPGVYWTGNDRIISQLTMMGPTR--LTLEEMDSMGDKRTALYEFTVONE 341

Oy 248 TRFFMHLGRISGNAGDAF-----RGLAKEDN----QNAMPSTSDVDNGCRPACLVNQO 299
 :: :: : | | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 342 ANKYOLSVSKYKGTLGGANLLIGASQVLVEGMTMTIHNSMFSTYDRDMDGWKIT- - --D 396

Oy 300 SVKSCSLHNHTGMWFNECGLANLINGIHFESGKL-----LATGIOMGTWTKNNSPVK 351
 || || | | | | | | | | | | : | : | : | : | : | : | : | : | : | : | :
Db 397 PRKCCK- EDDGGWMYNCHAAHPNGRITYWGCAITWDMAKTGDGVVMNMV---QGSHYS 453

Oy 352 IKVSMSKIRRMYPPE 367
 : | : | | | | | | | : | : | : | : | : | : | : | : | : | : | : | :
Db 454 MKKMskir---PYE 465

RESULT 6
FeHUB
fibrinogen beta chain precursor [validated] - human
N:Alternate names: coagulation factor I
N:Contains: fibrinopeptide B
C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence_revision 31-Mar-1993 #text_change 08-Dec-2000
C:Accession: BA3568; A90469; B90468; I37389; A94433; A90437; A94309; G54223; A03121;
R:Chung, D.W.; Harris, J.E.; Davile, E.W.
A>Title: Nucleotide sequences of the three genes coding for human fibrinogen.
A:Reference number: A43568; MUID:91344740; PMID:2102623
A:Accession: BA3568
A:Molecule type: DNA
A:Residues: 9-191,'P',193-491 <CHUD>
B:Chung, D.W.; Que, R.G.; Rixon, M.W.; Mace Jr., M.; Davile, E.W.
Biochemistry 22, 3244-3250, 1983
A>Title: Characterization of complementary deoxyribonucleic acid and genomic deoxyribo-
nuclease digestion products of the 5'-flanking region for the human fibrinogen beta gene
A:Reference number: A90469; MUID:83283433; PMID:6688356
A:Accession: A90469
A:Molecule type: DNA
A:Residues: 1-38 <CHU>
A:Accession: B90469
A:Molecule type: mRNA
A:Residues: 9-191,'A',193-491 <CH2>
A:Cross-references: GB:J00129; NID:g182429; PIDN:AAB52429.1; PID:g182430
R:Huber, P.; Dalmon, T.; Courtols, G.; Laurent, M.; Assouline, Z.; Marguerite, G.
Nucleic Acids Res. 15, 1615-1623, 1987
A>Title: Characterization of the 5'-flanking region for the human fibrinogen beta gene
A:Reference number: I37389; MUID:87146483; PMID:3029722
A:Accession: I37389
A>Status: translated from GR/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-38 <HUB>
A:Cross-references: EMBL:X05018; NID:g31400; PIDN:CAA28674.1; PID:g31401
R:Henschel, A.; Lottspeltch, F.; Southan, C.; Topfer-Petersen, E.
In Protides of the Biological Fluids, Proc. 28th Collqg., Peeters, H., ed., pp.51-56,
Artile: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural
features
A:Reference number: A94433
A:Contents: carbohydrate binding
A:Accession: A94433
A:Molecule type: protein
A:Residues: 31-137,'OS',140-144,'OF',147-491 <HEN>
R:Matt, K.W.K.; Takagi, T.; Doppelftelle, R.F.
Biochemistry 18, 768-76, 1979
A>Title: Amino acid sequence of the beta chain of human fibrinogen.
A:Reference number: A90437; MUID:79124640; PMID:420779
A:Accession: A90437
A:Molecule type: protein
A:Residues: 31-144,'OF',147-231,'D',233-330,'E',333-491 <WAT>
R:Bloomberg, B.; Hessel, B.; Hoggs, D.
Thromb. Res. 8, 639-658, 1976
A>Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
A:Reference number: A94309; MUID:76225080; PMID:936168
A:Contents: disulfide bonds
A:Accession: A94309
A:Molecule type: protein

A:Molecule type: mRNA
A:Residues: 276-437 <KAN>
R:Forname J.R., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.
J. Biol. Chem. 259, 12826-12830, 1984
A:Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near the
A:Reference number: A92448; MUID:85030379; PMID:6092346
A:Accession: B92448
A:Molecule type: DNA
A:Residues: 286-437 <FOR>
R:Man, A.M.A.; Eaton, M.A.W.; Williamson, R.; Humphries, S.
Nucleic Acids Res. 11, 7427-7434, 1983
A:Title: Isolation and characterization of cDNA clones for the alpha- and gamma-chains
A:Reference number: I37393; MUID:84069777; PMID:6689067
A:Accession: I37393
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 209-270 <RES>
R:Bernagoli, M.E.; Beckele, W.C.
J. Cell Biol. 121, 1329-1342, 1993
A:Title: Evidence for the selective association of a subpopulation of GPIIb-IIIa with th
A:Reference number: A40698; MUID:93286185; PMID:8509453
A:Accession: A40698
A:Molecule type: protein
A:Residues: 27-33, 'XX', 36-41 <BER>
A:Experimental source: thrombin-activated platelets
A:Note: sequence extracted from NCBI backbone (NCBI:133734)
R:Kuntzake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.
Biochemistry 33, 1988-1993, 1994
A:Title: Identification of proteins associated with apolipoprotein A-I-containing lipop
A:Reference number: A54223; MUID:94162201; PMID:8117655
A:Accession: H54223
A:Molecule type: protein
A:Residues: 27-33, 'XX', 36-41 <KUN>
A:Note: Identification of tryptic peptides from high-density lipoproteins
R:Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.
Ann. N. Y. Acad. Sci. 408, 28-43, 1983
A:Reference number: A90037; MUID:83254370; PMID:6575689
A:Contents: annotation; review; fibrinogen, disulfide bonds
R:Doolittle, R.F.; Takagi, T.; Watt, K.; Bouma III, H.; Cottrell, B.A.; Cassman, K.G.; C
in Regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S., Ottesen, M., Folt
A:Title: The structures of fibrinogen and fibrin.
A:Reference number: A94437
R:Blomback, B.; Hessel, B.; Hogy, D.
Thromb. Res. 8, 639-658, 1976
A:Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
A:Reference number: A94309; MUID:76225080; PMID:936108
A:Contents: annotation; disulfide bonds
R:Hoepflich, P.D.; Doolittle, R.F.
Biochemistry 22, 2049-2055, 1983
A:Title: Dimeric half-molecules of human fibrinogen are joined through disulfide bonds
A:Reference number: A90467; MUID:8321465; PMID:6860649
A:Contents: annotation; quaternary structure, disulfide bonds
R:Doolittle, R.F.
Annu. Rev. Biochem. 53, 195-229, 1984
A:Title: Fibrinogen and fibrin.
A:Reference number: A90041; MUID:84305751; PMID:6383194
A:Contents: annotation; review, EM structure, polymerization, ligands
R:Horwitz, B.H.; Varadi, A.; Scheraga, H.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 5980-5984, 1984
A:Title: Localization of a fibrin gamma-chain polymerization site within segment Thr-374
A:Reference number: A94006; MUID:85014892; PMID:6592597
A:Contents: annotation; polymerization region
R:Kloczewiak, M.; Timmons, S.; Lukas, T.J.; Hawiger, J.
Biochemistry 23, 1767-1774, 1984
A:Title: Platelet receptor recognition site on human fibrinogen. Synthesis and structure
A:Reference number: A90483; MUID:84203545; PMID:6326808
A:Contents: annotation; platelet aggregation region
R:Plow, E.F.; Srouji, A.H.; Meyer, D.; Margerite, G.; Ginsberg, M.H.
J. Biol. Chem. 259, 5388-5391, 1984
A:Title: Evidence that three adhesive proteins interact with a common recognition site o

A:Reference number: A92477; MUID:84185664; PMID:6325435
A:Contents: annotation; platelet aggregation region
R:Dang, C.V.; Ebert, R.F.; Bell, W.R.
J. Biol. Chem. 260, 9713-9719, 1985
A:Title: Localization of a fibrinogen calcium binding site between gamma-subunit post
A:Reference number: A92549; MUID:85261382; PMID:3160702
A:Accession: A92549
A:Contents: annotation; calcium binding region
R:Kirschbaum, N.E.; Budzynski, A.Z.
J. Biol. Chem. 265, 13669-13676, 1990
A:Title: A unique proteolytic fragment of human fibrinogen containing the alpha COOH
A:Reference number: A37117; MUID:90337977; PMID:2143188
A:Contents: annotation; hementin cleavage site
A:Note: hementin, a protease from Haemophilus phagocytans, the giant South American l
C:Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cle
ization sites responsible for the formation of the soft clot.
C:Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin stab
ger) and between alpha chains (weaker) of different monomers.
C:Comment: All fibrinogen chains are synthesized in the liver.
C:Comment: The two forms of gamma chain, A and B (see PIR:FGHGB), arise by alternate
intron, which makes this chain different from the gamma-B chain at positions 434-437
C:Genetics:
A:Gene: GDB:FCG
A:Cross-references: GDB:119132; OMIM:134850
A:Map position: 4q28-4q28
A:Introns: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1; 433/3
C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR
ins are contained in the core. Two three-chain coiled coils emerge from this core and
from the distal domain nodes.
C:Function:
A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized in
A:Pathway: blood coagulation
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C:Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprote
E:1-26/Domain: signal sequence #status predicted <SIG>
E:27-437/Product: fibrinogen gamma A chain #status experimental <MP>
E:116-415/Domain: fibrinogen beta/gamma homology <BG>
E:341-355/Domain: calcium binding #status predicted <CB>
E:400-422/Region: polymerization site, binding to the amino end of the alpha chain of
E:423-437/Region: platelet aggregation site, status predicted
E:161/Disulfide bonds: interchain (to gamma-35) #status experimental
E:35/Disulfide bonds: interchain (to gamma-34) #status experimental
E:43/Disulfide bonds: interchain (to beta-110) #status experimental
E:49/Disulfide bonds: interchain (to alpha-64) #status experimental
E:78/Binding site: carbohydrate (asn) (covalent) #status experimental
E:161/Disulfide bonds: interchain (to beta-227) #status experimental
E:165/Disulfide bonds: interchain (to alpha-180) #status experimental
E:179-208,352-365/Disulfide bonds: #status experimental
E:424/Cross-link: isopeptide (Gln) (interchain to Lys-432 N6-amino) #status experimen
E:432/Cross-link: isopeptide (Lys) (interchain to Gln-424) #status experimental
Query Match 18.68; Score 371.5; DB 1; Length 437;
Best Local Similarity 31.98; Pred. No. 6.6e-22;
Matches 105; Conservative 42; Mismatches 129; Indels 53; Gaps 11;
QY 65 NSIVSYRSTKTLKLNMDQ-----QASIDYLSNOYNEIENRVLTLTVEFRKQIDPF 118
DB 103 NMIDAATLTKSRKMLEIKWEASTILTHDSSIRYLQEIYNSNQNIVNKEV--AQLEAQ 160
QY 119 PHRP-----VQSH---GLDCTDIKPTIGSVYTPGCLYIHERGSSYPPEVWCMDYRGG 171
DB 161 QCEPCKDTIVQIHDITGKCCD-----INKGAKQSGLYFIKPLKANOQFLVYCEIDSGNG 216
QY 172 WTVQKRIIDGIIIDRBLMDVLDGFGD-----LGEFNLGKIKFYINQKTSMLVYAL 227
DB 217 WTVQKRIIDGIIIDRBLMDVLDGFGD-----LGEFNLGKIKFYINQKTSMLVYAL 276
QY 228 ESEDDTIAYASYNDFWEDTRFKMLGRYS--GNAGDAFRLKRED-----NONAM 278
DB 277 EDWNGRISTADYAMFKVGPEDAKYRLVAYAGDAGAFDGPDDSPDKPFTSHNGM 336
QY 279 PFSTSDVDNDCGRACLVNGQSVASCSHLNKTGWMEFECGLANGLIHRSGLN----- 333
DB 337 QFSTWMDNDKFEKGNCAEDQGS-----GWMNKKCHAGHLNGVYOGGTYSKAST 385

OY 334 ---LATGIOMGTWTKNNSPVKIKSVSMKI 359
Db 386 PNGYDNGIIMATW--KTRWYSMKKTMTMKI 412

RESULT 8
FGBHUB
fibrinogen gamma-B chain precursor [validated] - human
N/Alternate names: coagulation factor I; fibrinogen gamma-55 chain
C/Species: Homo sapiens (man)
C/Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 08-Dec-2000
C/Accession: A90494; A92448; A90453; A28203; B28203; I37390; A03126
R/Rikun, M.W.; Chung, D.W.; Davie, E.W.
Biochemistry 24, 2077-2086, 1985
A/Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.
A/Reference number: A90494; MUID:85252774; PMID:2990550
A/Accession: A90494
A/Molecule type: DNA
A/Residues: 1113,'T',115-453 <RIX>
A/Cross-references: GB:M10014; GB:J00134; GB:J00135; GB:X00086; NID:9182438; PIDN:AA8595
R/Fornace Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.
J. Biol. Chem. 259, 12826-12830, 1984
A/Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near the
A/Reference number: A92448; MUID:85030379; PMID:6092346
A/Accession: A92448
A/Molecule type: DNA
A/Residues: 286-453 <FOR>
R/Mollenstein-Yodel, C.; Moseson, M.W.
Biochemistry 20, 6146-6149, 1981
A/Title: Carboxy-terminal amino acid sequence of a human fibrinogen gamma-chain variant
A/Reference number: A90453; MUID:82068933; PMID:7306501
A/Accession: A90453
A/Molecule type: protein
A/Residues: 411-434,'Y',436-440,'Z',442,'Z',444,'B',446-447,'R',449,'ZBB',453 <MOL>
R/Francis, C.W.; Mueller, E.; Henschen, A.; Simpson, P.J.; Marder, V.J.
Proc. Natl. Acad. Sci. U.S.A. 85, 3358-3362, 1988
A/Title: Polymorphism of the human gamma chain fibrinogen gene.
A/Reference number: A94194; MUID:86217900; PMID:3368448
A/Accession: A28203
A/Molecule type: protein
A/Residues: 433-449 <FRA>
A/Accession: B28203
A/Molecule type: protein
A/Residues: 433-453 <FR2>
R/Marchetti, L.; Zanelli, T.; Malcovati, M.; Tenchini, M.L.
DNA Seq. 1, 419-422, 1991
A/Title: Polymorphism of the human gamma chain fibrinogen gene.
A/Reference number: I37390; MUID:92119334; PMID:1685103
A/Accession: I37390
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 75-286 <RES>
A/Cross-references: EMBL:X51473; NID:931410; PIDN:CAA3837.1; PID:9930064
C/Comment: The two forms of gamma chain, A (see PIR:FGHUG) and B, arise by alternate splicing, which makes this chain different from the gamma-B chain at positions 434-437 and C/Comment: The gamma-B chain is present in about 10% of the fibrinogen molecules in plas
C/Genetics:
A/Genes: GDB:FCG
A/Cross-references: GDB:119132; OMIM:134850
A/Map position: 4q28-q28
A/Introns: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1
C/Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FGHUG) and beta chains in the core. Two three-chain coiled coils emerge from this core and coiled from the distal domain ends.
C/Function:
A/Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
A/Pathway: blood coagulation
C/Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C/Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprotein;
F:1-76/Domain: signal sequence #status <SIG>
F:27-453/Product: fibrinogen gamma-B chain #status experimental <MPY>
F:176-415/Domain: fibrinogen beta/gamma homology <FBG>

F:341-355/Domain: calcium binding #status predicted <CAB>
F:400-422/Region: polymerization site, binding to the amino end of the alpha chain of
F:34/Disulfide bonds: interchain (to gamma-35) #status predicted
F:35/Disulfide bonds: interchain (to gamma-34) #status predicted
F:45/Disulfide bonds: interchain (to beta-110) #status predicted
F:49/Disulfide bonds: interchain (to alpha-64) #status predicted
F:78/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:161/Disulfide bonds: interchain (to beta-227) #status predicted
F:165/Disulfide bonds: interchain (to alpha-180) #status predicted
F:179-208,352-365/Disulfide bonds: #status predicted
F:424/Cross-link: isopeptide (Gln) (interchain to Lys-432 N6-amino) #status predicted
F:432/Cross-link: isopeptide (Lys) (interchain to Gln-424) #status predicted

Query Match 18.6%; Score 371.5; DB 1; Length 453;
Best Local Similarity 31.9%; Pred. No. 6; 9e-22;
Matches 105; Conservative 42; Mismatches 129; Indels 53; Gaps 11;

OY 65 NSIVSTRSTKKLLRMMEQ-----QASDLYLSNOVVELMNRVLLTTEVFRKQLDPF 118
Db 103 NMIDAATLRSKMLERIMKYEISILTHDSIRYLOEIVYNSNOKIVNLEKY--AOLEXQ 160
OY 119 PHRP---VQSH---GLDCTDIKDTIGSVTKPSGLYIHPGSSVPEFVCMDDYRGSG 171
Db 161 CQEPCKDTYQHIDYKDCQD---IANKGASGLYFIPKLANQFLVYCEIDSGSG 216
OY 172 WTVIQKIDIGIIDFORLWCDYLDGFGDL---LGEFWLGLKRIFYIVNOKNTSMLYVAL 227
Db 217 WTVFQKRLDGSVDYFKNNWIOYKEGFGHLSPTGTTERWLGNEKHILISTQALPYALRVEL 276
OY 228 ESEDDPLAAASDNFPLDEBTREFFKHLGRYS-GNAGDAFRLKED-----NONAM 278
Db 277 EWMNGRTSTADYAMFVGEADKRYLTAYVFAAGDAGDFDFGDDPSDKFFTSNMG 336
OY 279 PESTSDVDNDGCRPACTLVAGOSVKSCHLNKTKGFMFNCGLANLNGIHFFSGKL----- 333
Db 337 QSTWMDNDKREKGNABEDGS-----GWMNKHCHGHLNGVYOGGTYSKAST 385

OY 334 ---LATGIOMGTWTKNNSPVKIKSVSMKI 359
Db 386 PNGYDNGIIMATW--KTRWYSMKKTMTMKI 412

RESULT 9
A38463
fibrinogen beta chain - chicken (fragment)
C/Species: Gallus gallus (chicken)
C/Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 13-Aug-1999
R/Welssbach, L.; Oddoux, C.; Procyk, R.; Grieninger, G.
Biochemistry 30, 3290-3294, 1991
A/Title: The beta chain of chicken fibrinogen contains an atypical thrombin cleavage
A/Reference number: A38463; MUID:91182745; PMID:2009266
A/Accession: A38463
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-463 <WEL>
A/Cross-references: GB:M58514; NID:9211779; PIDN:AAA48770.1; PID:9211780
C/Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disu
F:73-202/Domain: fibrinogen disulfide ring homology <FDR>
F:212-460/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 18.6%; Score 371.5; DB 2; Length 463;
Best Local Similarity 27.7%; Pred. No. 7; 1e-22;
Matches 112; Conservative 57; Mismatches 136; Indels 99; Gaps 17;

OY 41 CEESCDVTKTKIREKHF--MGRNIONSLVST--TRSTKKLLRMND----- 83
Db 80 CPTGELDTTLKOKETVPRVLDKDRVAKESDSTWYQYVNMIDNKLVTOKORKDN 139
OY 84 -----EQGASLDLYLSNOVVELMNRVLLTTEVFRKQLDPFPHRPVS----- 125
Db 140 DILLSEYNTMELHNYIKDINDNNIPSSLRVLAIVDSL-HKTKQLENAIATOTDYCR 198

126 -----HGLDCTDIKDTIGSTKTPSGIYIIHPBESSYPFEVCMCDYRGGGT 173
199 SPVCASCNIPVSGRECEDEYIRKGET-----SEMYIIOPDEFTPYRYKCMETDNGMT 254
174 VIOKRIGDIIDFORLMCDYLDGFG-----DLGFEFLGLKTFYIVNOKNTSFM 222
255 LIQNRQGSVNFAGAMEYKRGFONIAKSGKKYCDIPGEVLGNDKISQITKGPFR-- 312
223 LYYALESED---DTLAYASDNFWLEDETRFEKMLHGRYSGNADAF---RGLKEDN- 274
313 --VLIEMEDWNGDKVS-ALYCGFTIHNEGNKYQLSVSNYKGNAGNALMEGASQLYGENRT 369
275 ---QNAPEFSDVDNDCGRPACLYNGOSVASCCHLNKTKWMEGCLANGLIHHSFG 331
370 MTIHNGMYFSTYDRDNG-----WLTDPDRKQCSK-EDGGGGMWYNRCHAAPNNGRYWGG 423
332 KL-----LATGIQGTWTKNNSPVKIKSVSKIRMYNPF 367
424 TYSMDAKHGTDCIYVMNM--KGSWYSKMKMSKIK----PYF 461

RESULT 10

A25052
fibrinogen beta chain - sea lamprey (fragments)
N:Contains: fibrinopeptide B
C:Species: Petromyzon marinus (sea lamprey)
C>Date: 25-Oct-1987 #sequence_revision 19-Feb-1999 #text_change 13-Aug-1999
C/Accession: A25052; A03124; B03124
R:Bohonus, V.L.; Doolittle, R.F.; Pontes, M.; Strong, D.D.
Biochemistry 25, 6512-6516, 1986
A>Title: Complementary DNA sequence of lamprey fibrinogen beta chain.
A:Reference number: A25052; MUID:87076582; PMID:3790537
A:Accession: A25052
A:Molecule type: mRNA
A:Residues: 39-479 <BOH>
A:Cross-references: GB:M14773; NID:g213191; PIDN:AAA49261.1; PID:g213192
R:Cottrell, B.A.; Doolittle, R.F.
Blood. Biophys. Acta 453, 426-438, 1976
A>Title: Amino acid sequences of lamprey fibrinopeptides A and B and characterization of
A:Reference number: A03120; MUID:77065679; PMID:999898
A:Accession: A03124
A:Molecule type: protein
A:Residues: 1-36 <COT1>
A:Accession: B03124
A:Molecule type: protein
A:Residues: 37-42 <COT2>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide
C:Keywords: blood coagulation; glycoprotein; sulfoprotein
F:1-36/Product: fibrinopeptide B #status experimental <FBP>
F:37-479/Product: fibrin beta chain #status experimental <MAT>
F:90-219/Domain: fibrinogen disulfide ring homology <FBG>
F:229-477/Domain: fibrinogen beta/gamma homology <FBG>
F:13/Binding site: sulfate (TYR) (covalent) #status experimental
F:27/Binding site: carbohydrate (ASN) (covalent) #status experimental

Query Match 18.5%; Score 370; DB 2; Length 479;
Best Local Similarity 28.9%; Pred. No. 9.7e-22;
Matches 108; Conservative 63; Mismatches 137; Indels 66; Gaps 17;

25 NAKESKSNITVCKEDE-----ESCQYKTKITREKHPKCRNLONSIVSTYRS 73
130 NSFDPMASDSWTLLKQNVOTLRRRLNSSSTHVNNAKELENRYKKEVKIR-ESTVAGSLRS 188
74 TKLLRMNMEQOASLDYLSNQVNELMNRVLLTTEVFRKQLDPEPRPVQSHGLDCTDI 133
189 MKSVLEHLRAKMQRMERAIKTQ-KELCSAPCTVACRY-----PVYS-GMHCEDI 235
134 KDTIGSTKTPSGIYIIHPBESSYPFEVCMCDYRGGGTIVIOKRIGDIIDFORLMCDYL 193
236 YRNGGRSTSEA---YTIQPDLFSEPRYKVFCDMESHGGGVTVQNRVDSSTNFARDWMYTK 291
194 DGFCDL-----GEFWLGLKTFYIVNOKNTSFMLYVALESDDTLAASYNF 242

292 AEFNINAFNGNKSICNIPGEWLGTKYHQLTKO-HIQOVLFDMSDWEGSSV-YAQYASF 349
243 WLEDETRFEKMLHGRYSGNADAF-FRGLK--EDNQ-----NAMPFSTDVNDGCRPAC 294
350 RPEMDAQYRLWVEDYSGNAGNALLLEGATOLMGDRWRTIHNGQFSTFDDNDNMNM-- 407
295 LVNGOSVASCCHLNKTKWMEGCLANGLIHHSFG---KLA-----TGIQGTWTKN 346
408 ---GDPETHKCSR-EDAGGGMWYNRCHAAPNNGRYWGGIYTRKQADYCTDGDGVVMNM--K 461
347 NSPVKIKSVSKIR 360
462 GSWYSKMKMKLR 475

RESULT 11

S05313
fibrinogen gamma-B chain precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Aug-1999
C/Accession: S05313
R:Brown, W.M.; Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R.
Nucleic Acids Res. 17, 6397, 1989
A>Title: Nucleotide and deduced amino acid sequence of a gamma subunit of bovine fibrinogen
A:Reference number: S05313; MUID:8936676; PMID:2711651
A:Accession: S05313
A:Molecule type: mRNA
A:Residues: 1-444 <BRO>
A:Cross-references: EMBL:X15556; NID:g349; PIDN:CAA33562.1; PID:g350
A>Note: The authors translated the codon AGT for residue 105 as Ala and ART for resid
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-444/Product: fibrinogen gamma-B chain #status predicted <MAT>
F:174-414/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 18.2%; Score 365; DB 2; Length 444;
Best Local Similarity 30.2%; Pred. No. 2.2e-21;
Matches 100; Conservative 51; Mismatches 124; Indels 56; Gaps 12;

65 NSIYSTRSTKLLRNMM-----DEQOASLDYLSNQVNELMNRVLLTTEVFRKQLDPE 118
101 NNIESATNKSMSMEIKYETLISTHETRFLOEYVNSQKIVNLRDLYV--QLEAN 158
119 PHRPVQ-----HGLDCTDIKDTIGSVTKTPSGIYIIHPBESSYPFEVCMCDYRGGG 171
159 QCEPQODTVKIDHTYGRQCD---VANKGAKESGLYTRPL-KAKQFLYVCEIDSGSG 213
172 WTIVQKRIGDIIDFORLMCDYLDGFGDL-----GEFWLGLKTFYIVNOKNTSFMLYV 225
214 WTVQKRIGDSIDPRKKNIOYKEGSHLSPGTGTETFWLNEKIHILISTOSIIPYVLR 273
226 ALSEDDTLAASYNFWLEDETRFEKMLHGRY-SGNAGDAFRGLKEDN-----NQN 276
274 QLEDMNGTSTADYASFVYTGENDKIRLTLYVFGGDDGDFDGDGDDSSDKFFTSYHN 333
277 AMPFSTDVDNDGCRPACLYNGOSVASCCHLNKTKWMEGCLANGLIHHSGLKLTAT 336
334 GMPSTWMSQNDKDKDNC---AEQY-----GIGWMNMKCHAGHLNGVYUUGGTYSKT 382
337 -----GIQGTWTKNNSPVKIKSVSKIR 359
383 STPNGYDNGIIMATW--KSRWYSKMKTKYTKI 411

RESULT 12

FGIMGs
fibrinogen gamma chain precursor - sea lamprey
C:Species: Petromyzon marinus (sea lamprey)
C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 20-Oct-2000
C/Accession: A03129
R:Strong, D.D.; Moore, M.; Cottrell, B.A.; Bohonus, V.L.; Pontes, M.; Evans, B.; Rlie
Biochemistry 24, 92-101, 1985
A>Title: Lamprey fibrinogen gamma chain: cloning, cDNA sequencing, and general charac

A:Reference number: A03129; MUID:85199776; PMID:2581603
A:Accession: A03129
A:Molecule type: mRNA
A:Residues: 1-432 <STR>
A:Cross-references: GB:K03049; NID:9213193; PIDN:AAA49262.1; PID:9213194
C:Keywords: fibrinogen gamma chain; fibrinogen beta/gamma homology
C:Keywords: blood coagulation; glycoprotein; liver; plasma; pyroglyutamic acid
F:1-24/Domain: signal sequence #status predicted <SIG>
F:125-432/Product: fibrinogen gamma chain #status experimental <MP>
F:175-411/Domain: fibrinogen beta/gamma homology <FBG>
F:225/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
F:227/Binding site: carboxylate (Asn) (covalent) #status predicted
F:421/Cross-link: isopeptide (Gln) (interchain to Lys-425 N6-amino) #status predicted
F:425/Cross-link: isopeptide (Lys) (interchain to Gln-421) #status predicted

Query Match 18.0%; Score 360; DB 1; Length 432;
Best Local Similarity 30.1%; Pred. No. 5, 3e-21;
Matches 115; Conservative 52; Mismatches 151; Indels 64; Gaps 16;

QY 13 DSSVNVIVEDGSNAKDE-SKSNIDYCKEDCEESCVKTKITREKIFKCRNLQNSIVSYT 71
DB 62 DSSFDISVLTQLAAKHGIVEGVNIVNED-----VITTRDEAQIINDSGQKTYQKIL 113
QY 72 RSTKLLRNMBDEQASLDYLS-----NQ--VNELNRRVLLLTTEYFRKOLDFPHRPVQ 124
DB 114 EEV-RILEDIGVSHDAQIELSEMRVNOQFYTRLQOQLVDIRQTSRSCQDTANKISP 172
QY 125 SHGLDCTDIKDTIGSYTKTPSGLYIITHPGSSYFEVWCDMDYRGSGWTVIQKRIDGIID 184
DB 173 IKGKDCQGVVDNGK-----DSGLYIKPLKAKQPLVECEIE-NGNGMTVIOIQRHDSGVN 227
QY 185 FORIMCDYLDGFG-----DLGFEWLGKIKFIYVNOKNKNSFMYLVLESDDTLAAASYD 240
DB 228 FTRDMVSTREGGYLAPLTTLTFEWSGNEKIHILTGQO--AYRLIDLDTWMENTHRADYG 285
QY 241 NFWL--EDETFR-FKMHIGRYSNAGDAFRGLKEDNON-----AMFESTDVND 288
DB 286 HRRKLPRSEDEYRLFYSMYL--DGDGNAFNDFDEGDDQDKFYTHLGLMSTPERDND 342
QY 289 GCRPACLVNGQSVKSCSHLHNTGWMFNEGGLANLNGIHHSFKLLAT-----GIOM 340
DB 343 KYEGSCAEODGS-----GWMNMRCHAGHLNGKYFGGNRYKRTDVEFPYDGGIIM 391
QY 341 GWTNKNNSPVKIKSVSMKIRRM 362
DB 392 ATW--HDMRYSLKMTTKLLPM 411

RESULT 13
A32670
fibrinogen gamma chain - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 13-Aug-1999
C:Accession: A32670; I51416
R:Pastori, R.L.; Moskaitis, J.E.; Smith Jr., L.H.; Schoenberg, D.R.
Biochemistry 29, 2599-2605, 1990
A:Title: Estrogen regulation of Xenopus laevis gamma-fibrinogen gene expression.
A:Reference number: A32670; MUID:90241882; PMID:2334684
A:Accession: A32670
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-438 <PAS>
A:Cross-references: GB:J02894; NID:9214139; PIDN:AAA49709.1; PID:9214140
R:Bhattacharya, A.; Shepard, A.R.; Moser, D.R.; Holland, L.J.
Mol. Cell. Endocrinol. 72, 213-220, 1990
A:Title: Isolation and characterization of cDNA clones for the gamma subunit of Xenopus
A:Reference number: I51416; MUID:91146806; PMID:2289632
A:Accession: I51416
A:Status: preliminary
A:Molecule type: translated from GB/EMBL/DBJ
A:Residues: 1-58 <SHA>
A:Cross-references: GB:M35548; NID:9214141; PIDN:AAA03247.1; PID:9214142
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology

C:Keywords: blood coagulation
F:173-413/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 17.6%; Score 352.5; DB 2; Length 438;
Best Local Similarity 27.2%; Pred. No. 2, 2e-20;
Matches 106; Conservative 54; Mismatches 141; Indels 89; Gaps 14;

QY 39 EDCEESCVKTKITREKIF-----MCRNLQNSIVSYTSTKLLRNMD-----EQQ 86
DB 41 EYCPPTGIGISDFLNRYQENVDDQLQLEMLNQINSSTGTTIIVHLIDSGKRPATSPQ 100
QY 87 ASLD-----YLSNVNELMNRVLLLTTEYFRKQD-FF 118
DB 101 TADPMTQSKTCMKLTDMKNYYQYEENILYQEVYSSNQNKIFLKKRIANLELQCOQ 160
QY 119 PRRPV-----QSHGLDCTDIKDTIGSYTKTPSGLYIITHPGSSYFEVWCDMDYRGSGWT 174
DB 161 PCGDDYQIQEFTKDCQGEVANKGARL-----SGLYIKPLKAKQPLVECEIESGSMATV 216
QY 175 IOKRIDGIIDFORIMCDYLDGFGDL-----LGEFWLGKIKFIYVNOKNKNSFMYLVLESE 230
DB 217 IORRLDGSVNFHKNNVQYREGFGLSPNDKTFEWSGNEKIHILSTQSTIPYVRIELEDM 276
QY 231 DDTLAAASYDNFWL--EDETFR-FKMHIGRYSNAGDAFRGLKED-----NQNM 278
DB 277 SNKSTADYSTFLGSEKDNRYFTYVFTG--GDAGDAFDGDFGDDSDKFTYSHNGM 333
QY 279 PFSTSDVNDGCRPACLVNGQSVKSCSHLHNTGWMFNEGGLANLNGIHHSFKL----- 333
DB 334 QFSTFKDNDKFDGCAEODGS-----GWMNMRCHAHNLNGKYGGGTYSADS 382
QY 334 ----LATGIOMGWTNKNNSPVKIKSVSMKI 359
DB 383 GPSGYDNGIIMATWRR--WYSKSVTKMI 410

RESULT 14
A35084
fibrinogen-related protein A precursor - sea cucumber (Parastichopus parvlenensis)
C:Species: Parastichopus parvlenensis
C:Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 09-Sep-1997
C:Accession: A35084
R:Xu, X.; Doolittle, R.F.
Proc. Natl. Acad. Sci. U.S.A. 87, 2097-2101, 1990
A:Title: Presence of a vertebrate fibrinogen-like sequence in an echinoderm.
A:Reference number: A35084; MUID:90192754; PMID:2315305
A:Accession: A35084
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-282 <XUX>
A:Cross-references: GB:M31326; NID:9161164; PID:9161165
C:Superfamily: fibrinogen beta/gamma homology
F:67-280/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 17.5%; Score 350.5; DB 2; Length 282;
Best Local Similarity 36.8%; Pred. No. 1, 8e-20;
Matches 92; Conservative 31; Mismatches 96; Indels 31; Gaps 10;

QY 113 KQLDPPRRPVQSHGLDCTDIKDTIGSYTKTPSGLYIITHPGSSYFEVWCDMDYRGSGM 172
DB 58 KRISHREYR-----HDCYDIIQSC-SGQSPSGQYIIPDDGNL-IRKYCMEIDEGW 110
QY 173 TVIQKRIDGIIDFORIMCDYLDGFGDLGFEWLGKIKFIYVNOKNKNSFMYLVLESEDD 232
DB 111 TVFORRIDGTINFRYSMYQTGFGNLNTEFWLGNNDIHYLNSQD--YELRVELNNTLG 168
QY 233 TLAYASYDNFWLEDERFRFKMLHGRYSNAGDAFRGLKEDNONAMPFSTSDVNDGCRP 292
DB 169 NHYAKYVNFRIQDSFSEFLVLAAGSAGPAGDSLA-----YHNMRFSTYDNDND---- 218
QY 293 ACLVNGQSVKSCSH-LAHNTGWMFNEGGLANLNGIH-HSGKLLATGIOMGWTNKNNSPV 350
DB 219 -----YSTINCASHSSYGGAMMYKSCLLSNLNGQYIYDYG--APSTIYWSILPDGND-- 268

QY	351	KIKSVSMKIR	360
	:	:	
Db	269	QIPFAEMKLR	278

RESULT 15

A39832
scabrous locus (sca) protein precursor - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 01-Dec-2000
C:Accession: A39832; S58998
R:Baker, N.E.; Mlodzik, M.; Rubin, G.M.
S:Science 250, 1370-1377, 1990
A:Title: Spacing differentiation in the developing *Drosophila* eye: a fibrinogen-related
A:Reference number: A39832; MUID:91075223; PMID:2175046
A:Accession: A39832
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-774 <BAK>
A:Cross-references: GB:M60065; GB:M37703; NID:g158401; PID:g158402
R:Hu, X.; Lee, E.C.; Baker, N.E.
Genetics 141, 607-617, 1995
A:Title: Molecular analysis of scabrous mutant alleles from *Drosophila melanogaster* ind
A:Reference number: S58998; MUID:96109607; PMID:8647397
A:Accession: S58998
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-18, 'T', 20-774 <HDX>
C:Genetics:
A:Gene: FlyBase:scra
A:Cross-references: FlyBase:FBgn000326
C:Superfamily: fibrinogen beta/gamma homology
F:514-711/Domain: fibrinogen beta/gamma homology <FBG>

Search completed: December 16, 2002, 17:36:22
Job time : 16.6032 secs

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OM protein - protein search, using sw model

Run on: December 16, 2002, 17:27:23 ; Search time 8.7619 Seconds

(without alignments)
1742.006 Million cell updates/sec

Title: US-09-596-196-9

Perfect score: 2000
Sequence: 1 EYVQGNVCHHSTDDSSVNVIV.....PVKIKSVSMKIRMTNPKYK 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	413.5	20.7	439	1	FGI2_HUMAN
2	405.5	20.3	432	1	FGI2_MOUSE
3	400.5	20.0	481	1	AGP1_BOVIN
4	400.5	20.0	493	1	AGP1_MOUSE
5	400	20.0	493	1	AGP2_MOUSE
6	398	19.9	312	1	FGI1_HUMAN
7	395.5	19.8	468	1	FGI1_BOVIN
8	395	19.8	498	1	AGP1_HUMAN
9	391	19.6	498	1	AGP1_MOUSE
10	381.5	19.1	496	1	AGP2_HUMAN
11	375.5	18.8	491	1	FGI1_HUMAN
12	375	18.8	375	1	FGI2_BOVIN
13	374.5	18.7	496	1	AGP2_MOUSE
14	373.5	18.7	479	1	FGI1_MOUSE
15	371.5	18.6	453	1	FGI1_HUMAN
16	371.5	18.6	463	1	FGI1_BOVIN
17	370	18.5	477	1	FGI1_MOUSE
18	365	18.2	444	1	FGI1_BOVIN
19	360	18.0	432	1	FGI1_MOUSE
20	360	18.0	509	1	AGP1_MOUSE
21	358	17.9	503	1	AGP1_HUMAN
22	352.5	17.6	438	1	FGI1_MOUSE
23	351	17.5	319	1	FGI1_MOUSE
24	350.5	17.5	282	1	FGI1_MOUSE
25	348.5	17.4	774	1	SCA_DROME
26	337.5	16.9	866	1	FGI1_HUMAN
27	335.5	16.8	741	1	FGI1_MOUSE
28	332	16.6	306	1	FGI1_MOUSE
29	329.5	16.5	641	1	FGI1_MOUSE
30	329	16.4	334	1	FGI1_MOUSE
31	327.5	16.4	445	1	FGI1_MOUSE
32	321.5	16.1	255	1	FGI1_MOUSE
33	321	16.1	255	1	FGI1_MOUSE

34	313.5	15.7	782	1	FGI1_MOUSE
35	310.5	15.5	1808	1	FGI1_MOUSE
36	308.5	15.4	326	1	FGI1_MOUSE
37	305.5	15.3	335	1	FGI1_MOUSE
38	302.5	15.1	4289	1	FGI1_MOUSE
39	291	14.5	289	1	FGI1_MOUSE
40	282.5	14.1	1746	1	FGI1_MOUSE
41	271	13.6	2201	1	FGI1_MOUSE
42	197	9.8	137	1	AGP2_MOUSE
43	109	5.5	129	1	AGP2_MOUSE
44	98	4.9	782	1	FGI1_MOUSE
45	97.5	4.9	1432	1	FGI1_MOUSE

ALIGNMENTS

RESULT 1
ID FGI2_HUMAN STANDARD; PRT; 439 AA.
AC 014314;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen precursor (Fibrinogen-like protein 2) (PT49).
GN FGI2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=95369700; PubMed=7642106;
RA Ruegg C., Pytela R.; transcript expressed in T-lymphocytes and
RT encoding a fibrinogen-like protein.";
RL Gene 160:257-262(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Yuvaraj S., Liu M., Marsden P., Levy G.;
RT "Cloning and characterization of Hfg12: the human counterpart to the
RT mouse gene Fgl2.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. AND VARIANT G1U-53.
RA Rieder M.J., Amel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RL Poel G.L., Ozuna M., Yi Q., Nickerson D.A.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=98309432; PubMed=9647217;
RA Marzetti S., Blum S., Hartmann R., Gundersen D., Schreyer M.,
RA Argaves S., von Fillechner V., Pytela R., Ruegg C.;
RT "Characterization of human fibrinogen, a fibrinogen-like protein
RT secreted by T lymphocytes.";
RL J. Immunol. 161:138-147(1998).
CC -!- FUNCTION: MAY PLAY A ROLE IN PHYSIOLOGIC LYMPHOCYTE FUNCTIONS AT
CC MUCOSAL SITES.
CC -!- SUBUNIT: HOMOTETRAMER. DISULFIDE-LINKED.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC
CC T-CELLS.
CC -!- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
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CC or send an email to license@isb-sib.ch).

DR EMBL: Z36531: CAA85298.1: -
DR EMBL: AF104015: AAD10825.1: -
DR EMBL: AF104014: AAD10825.1: JOINED.
DR EMBL: AF468959: AAL68855.1: -
DR HSSP: P02671: 1FZD.
DR Genew: HGNC:3696: FGL2.
DR MIM: 605351: -
DR InterPro: IPR002181: Fibrinogen_C.
DR Pfam: PF00147: Fibrinogen_C: 1.
DR SMART: SM00186: FBG: 1.
DR PROSITE: PS00514: FIBRIN_AC_C_DOMAIN: 1.
KW T-cell; Glycoprotein; Signal; Polymorphism.
FT SIGNAL 1 23
FT CHAIN 24 439
FT DOMAIN 210 435
FT DISULFID 213 242
FT DISULFID 371 384
FT CARBOHYD 25 25
FT CARBOHYD 179 179
FT CARBOHYD 235 235
FT CARBOHYD 263 263
FT CARBOHYD 336 336
FT VARIANT 53 53
SQ SEQUENCE 439 AA: 50228 MW: DF34656288E49E68 CRC64:
/FTID=VAR_013066.

Query Match 20.7%; Score 413.5; DB 1; Length 439;
Best Local Similarity 30.2%; Pred. No. 1.1e-25;
Matches 119; Conservative 61; Mismatches 147; Indels 67; Gaps 15;

OY 14 SSVVNIIVEDGSNAKDESKNDIVCKEDCE-----ESCDVKTK 50
DB 73 SIEEVFKFVQLKELVNSLKSC-QDCKLQADDNDEGRNLLPSTGAPGEVGNRR 131
OY 51 ITRREKHFMCRLQNS---IYSTRSTPKLLRNM-----MDEQASLDYLSNOVNEIM 100
DB 132 ELESEVNRKSSSELKNAKEINVLHGRLEKLNLYNNNIENYDSKAVNLFVYNSLDGKC 191
OY 101 NRVLLITTEVFRKQIDPPRPVQSHGL--DCTDIKDTIGSVTKPPSGLYTHPEGSSVP 158
DB 192 SGC-----PSOEIOISRPVQ-HLYTKCSDYV---AIGKSSSEYRVTPPPKNS 237
OY 159 FEVMCDMDYRGSGMTYIOKRIGTIDFORLWCDYLDGFGDLGEPFLGKTFEYIYNOKN 218
DB 238 FEVYCDMEFMGGWTVLAKRLDGSINFTFTWODYKAFGKFLRREMLGDKTHLLT--KS 295
OY 219 TSEFMLVALESEDDTLAVASYDNFMLEDETRFKMHLGRYSNAGDAFGLKKEQNOMN 278
DB 236 KEMILRIIDLEDENGVELVLYDOFYVANEFLYRLHVGNYGTAGDALR-FKHVNHDLK 354
OY 279 PSTSDVNDGCRPACLVNGQSVKSGSHLANKTGWFNFCGLANLNG-1HHSGLLATG 337
DB 355 FETTPDKNDKDRVPSG-----NCG-LYSSGWMFDCASLANLNGKYHOKYRGVRNG 404
OY 338 IOWGTW--TKNSSPVKIKSVKIRRMYP-YEK 368
DB 405 IFWGTWPGVSEAHPGCYKSKFEKAMKMPKHPK 438

RESULT 2
FGL2_MOUSE
ID FGL2_MOUSE STANDARD: PRT: 432 AA.
AC P12804.
DT 01-OCT-1989 (rel. 12, Created)
DT 01-OCT-1989 (rel. 12, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Fibrinolytic precursor (Fibrinogen-like protein 2) (Prothrombinase)
DE (Cytotoxic T-lymphocyte specific protein).
GN FGL2 OR FIBLP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cytotoxic T-cell;
RX MEDLINE=87175527; PubMed=3550794;
RA Koyama T., Hall L.R., Haseg W.G., Tonegawa S., Saito H.;
RT "Structure of a cytotoxic T-lymphocyte-specific gene shows a strong
RT homology to fibrinogen beta and gamma chains".
RL Proc. Natl. Acad. Sci. U.S.A. 84:1609-1613(1987).
RN [2]
RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=BA1B/CJ; TISSUE=Peritoneal macrophage;
RX MEDLINE=95333285; PubMed=7609073;
RA Parr R.L., Fung L., Reneker J., Myers-Mason N., Leibowitz J.L.,
RA Levy G.;
RT "Association of mouse fibrinogen-like protein with murine hepatitis
RT virus-induced prothrombinase activity".
RL J. Virol. 69:5033-5038(1995).
CC -1- FUNCTION: CONVERTS PROTHROMBIN TO THROMBIN.
CC -1- SUBUNIT: HOMOTETRAMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC
CC T-CELLS.
CC -1- INDUCTION: IN MACROPHAGES, DURING INFECTION BY MOUSE HEPATITIS
CC VIRUS STRAIN 3 (MHV-3).
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.

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CC or send an email to license@sdb.ch).

DR EMBL: M16238: AAA37624.1: -
DR EMBL: M15761: AAA37624.1: JOINED.
DR EMBL: S78773: AAB34823.1: -
DR PIR: A27447; A27447.
DR HSSP: P02671; 1FZD.
DR MGD: MGI:103266; Fgl2.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147: fibrinogen_C: 1.
DR SMART: SM00186: FBG: 1.
DR PROSITE: PS00514: FIBRIN_AC_C_DOMAIN: 1.
DR T-cell; Cytolysis; Signal.
FT SIGNAL 1 19
FT CHAIN 20 432
FT DOMAIN 203 428
FT DISULFID 206 235
FT DISULFID 364 377
FT CARBOHYD 24 24
FT CARBOHYD 172 172
FT CARBOHYD 228 228
FT CARBOHYD 256 256
FT CARBOHYD 329 329
FT CONFLICT 332 332
SQ SEQUENCE 432 AA: 48951 MW: 28297F69CDBA782 CRC64:
A->G (IN REF. 2).

Query Match 20.3%; Score 405.5; DB 1; Length 432;
Best Local Similarity 35.4%; Pred. No. 4.8e-25;
Matches 110; Conservative 43; Mismatches 115; Indels 43; Gaps 13;

OY 78 LRNMDEQA-----SLDYLSNOVNEIMNRVLLTTEVERKQID-----PP 119
DB 137 LKNNAKQDGLGRLETLHLVNNNIENYVDKVNLFVV--NSLDGKSCPSQEHMQ 194
OY 120 HRPVQSHGL--DCTDIKDTIGSVTKPPSGLYTHPEGSSYPPEVNCMDYRGSGMTYIOK 177
DB 195 SOPVO-HLYTKCSD-HVYLG--RRSSGAYRVTPDHRNSFEVYCDMEFMGGWTVLQ 249
OY 178 RIDGSIIFORLWCDYLDGFGDLGEPFLGKTFEYIYNOKNFSFMLVVALESDDTLAVA 237
DB 250 RIDGSIIFREMKDYKAGKGNLEFREFWLGNDKXIHLLT--KSKEMILRIIDLEDNGLTLXA 307

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QY 238 SYDNFWLEDETRFFKMHGKRYSGNAGDAFRGLKEDNONAMPSTSDVNDCCRPACLVN 297
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 308 LYDPOFYVANEFLKRYLRHIGNNGTAGDALR-FSRHYNDLFEFTTPDRDNRPSG---- 362
QY 298 GQSVKSCSHLNKRWMPNECCGLANLNG-IHFGSKLLATGICGWTWKKNN--SPVKIKS 354
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 363 -----NCG-LYSSGGMWDFSCLSANLNKGYHOKYGVGRNGIFWGTWGINQADPGGYKS 416
QY 355 VSMKIRRYNYP 365
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 417 SFRQAKMIRP 427

RESULT 3
AGP1_BOVIN STANDARD; PRT: 481 AA.
ID AGP1_BOVIN 018920:
AC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiopoietin-1 precursor (ANG-1) (Fragment).
GN ANGPT1 or ANG1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN 11
RP TISSUE=Ovary;
RC MEDLINE=99034348; PubMed=9840613;
RA Goede V., Schmidt T., Kimlina S., Kozian D., Augustin H.G.;
RT "Analysis of blood vessel maturation processes during cyclic ovarian
RT angiogenesis.";
RL Lab. Invest. 78:1385-1394(1998).
RN 12
RP SEQUENCE OF 91-200 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98451564; PubMed=9776732;
RA Mandriota S.J., Pepper M.S.;
RT "Regulation of angiopoietin-2 mRNA levels in bovine microvascular
RT endothelial cells by cytokines and hypoxia.";
RL Circ. Res. 83:852-859(1998).
CC -1- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS
CC TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
CC PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
CC CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
CC ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
CC VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
CC HEART EARLY DEVELOPMENT (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DEVELOPMENTAL STAGE: FOUND TO BE EXPRESSED THROUGHOUT THE OVARIAN
CC CYCLE.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF093573; AAC61872.1; -.
DR EMBL: AF032923; AAC78245.1; -.
DR HSSP: P02671; 1PZD.
DR InterPro: IPR002181; fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C.1.
DR SMART: SM00186; FBG.1.
DR PROSITE: PS00514; FIBRIN-AG C-DOMAIN.1.
KM Glycoprotein; Coiled coil; Signal.
FT SIGNAL 1 15 POTENTIAL.

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FT CHAIN 16 >481 ANGIOPOIETIN-1.
FT DOMAIN 153 261 COILED COIL (POTENTIAL).
FT DOMAIN 283 >481 FIBRINOGEN C-TERMINAL.
FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 243 243 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 481 481
SQ SEQUENCE 481 AA; 55556 MW; 8EEC9ED84FC2B850 CRC64;

Query Match 20.0%; Score 400.5; DB 1; Length 481;
Best Local Similarity 27.9%; Pred. No. 1,4e-24;
Matches 114; Conservative 60; Mismatches 116; Indels 119; Gaps 15;

QY 3 VQGNVHSTDTSSVYNIYEDSGSNMADESKSDNYVCKECCESQDYKTYTRKKHFMKRN 62
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 115 IQQNAVQNH-----ATMLEIGTSLSSQ-----AEQTRKLDVEYVLNQTSLRLYLQL 163
QY 63 LQNSIVSY-----TRSTKLLRNMM 82
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 164 LENSLSYTKLEKQQLQQTNEILKIHENKSLLEHKIFEMEGKHKELDYFKKEKENTLQGLY 223
QY 83 DEQASLDYLSQNV-----ELM-----NRYLLITVEVF-----RKQLDPP 119
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 224 TRQTYIIDLEKQILNRATTNNSVLOKQOLEMDYVHNLVNLCTKRVLLKGGKRREKPF- 282
QY 120 HRPVQSHGLDCTDIDKIGSVTKRPSGLYTHPESSYSPFEVCMCDMDRGGMVYQKRI 179
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 283 -----RDADVY-----QAGFNKSGIYTYIYINMPKPKVFCMDLNGSGWVYIQHRE 330
QY 180 DGIIDFORLMDYLDGFDGLGEFWLGLKIFYIVNQNTSPMLYVALESEDDTLAVASY 239
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 331 DGSIDFQGWKEKYGKGFENPSEGYWLGNEFFAITSQR--QYLRLELDMEGNATYQY 388
QY 240 DNFWEDETRFFKMHGKRYSGNAGDAFRGLKEDN--ONAMPSTSDVNDCCRPAC--L 295
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 389 DRFHIGNEKQVRYLYLKCHTGTAG-----KQSLILHGADEFSTKDDNDNCMCCKALM 441
QY 296 VNGQSVKSCSHLNKRWMPNECCGLANLNGIHHS-----GRLATGICGM 340
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 442 LFG-----GWMFDACGPSNLNGMFTYAGQNHKLU--NGIKW 475

RESULT 4
ANL2_MOUSE STANDARD; PRT: 493 AA.
ID ANL2_MOUSE 09R045:
AC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiopoietin-related protein 2 precursor (angiopoietin-1like 2).
GN ANGPTL2 OR ARP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN 11
RP TISSUE=Heart;
RC MEDLINE=99403103; PubMed=10473614;
RX Kim I., Moon S.-O., Koh K.N., Kim H., Uhm C.-S., Kwak H.J., Kim N.-G.,
RA Koh G.Y.;
RT "Molecular cloning, expression, and characterization of angiopoietin-
RT related protein. angiopoietin-related protein induces endothelial cell
RT sprouting.";
RL J. Biol. Chem. 274:26523-26528(1999).
CC -1- FUNCTION: INDUCES SPROUTING IN ENDOTHELIAL CELLS THROUGH AN
CC AUTOCRINE AND PARACRINE ACTION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEART, TONGUE, LUNG AND
CC SKELETAL MUSCLE. ALSO FOUND IN LOWER LEVELS IN KIDNEY, EPIDIDYMUS
CC AND TESTIS.

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CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF125176; AAD53538.1; -.
DR HSSP; P02671; 1FZD.
DR MGD; MG1:1347002; Angptl2.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Signal; Coiled coil; Glycoprotein.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 493 ANGIOPOIETIN-RELATED PROTEIN 2.
FT DOMAIN 77 115 COILED COIL (POTENTIAL).
FT DOMAIN 152 202 COILED COIL (POTENTIAL).
FT DOMAIN 438 450 FIBRINOGEN C-TERMINAL.
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 493 AA; 57118 MW; 22885ABEF0746BF2 CRC64;

Query Match 20.0%; Score 400.5; DB 1; Length 493;
Best Local Similarity 26.7%; Pred. No. 1.4e-24;
Matches 107; Conservative 66; Mismatches 107; Indels 121; Gaps 15;

QY 48 KTKITREKHEKMCNLTNSIVSTRSTKTLRMMDQQAISLYLSNOVVELNRRVLLLT 107
DB 119 EYKULRKES-----RNNNSRV---TOLYQMLHEITIKRDNAL-----ELSQLNRILINOT 166
QY 108 TEVER-----KOLD-----PEPHRP----- 122
DB 167 ADMLQASKYKDEHKEFOHMLAHNOSVIAQLEEHCKRVPARARMPQPPARAPRVYQ 226
QY 123 -----VQSH-----GLDCTDIKDTIGSVTKTPSG----- 146
DB 227 PPTYNRIINOISTNEIOSQONIKVLPPLPTMPALTSLSSTDKPSGPMWDCLOALEDHG 286
QY 147 ----LYIHPEGSSYFEYWCMDYRGGWTVYQKRIGIDFQRLMCDYLDGFGDLGE 202
DB 287 STSSITLVPRNTNRLMQWCDOHRDPGCVTYQKRIDGSVNFRRMVEYTKQSGFGNIDGE 346
QY 203 FVLGLKRIEYIVNOKNTSEMLYVALESEDDTLAASVDNFWLEDETRFEKMLGRYSGNA 262
DB 347 YMLGLENIYWLNGN--YKLLVTMEDWSGRKVFAYASFLPESEYKYKRLGRYHGN 404
QY 263 GDAFRGLKEDNONAMPSTSDVDNDCGRPACLVNCGSVKSCSHLNKKGWPNEGGLAN 322
DB 405 GGSFTW-----HNGKQFTTLDRDHD-----VYTG-----NCAH-YQKGGWVYNACASHN 447
QY 323 LINGIHFSGLLA---TGIONGTWTKNNSPVKIKSVSMKR 360
DB 448 LNCVWYRGGHYSRYODGVYMAEF--RGGSYSILKVVYMMIR 486

RESULT 5
ANL2_HUMAN
ID ANL2_HUMAN STANDARD; PRT; 493 AA.
AC 09UK09;
DT 16-OCT-2001 (rel. 40; Created)
DT 16-OCT-2001 (rel. 40; Last sequence update)
DT 15-JUN-2002 (rel. 41; Last annotation update)
DE Angiopoietin-related protein 2 precursor (Angiopoietin-like 2).
GN ANGPTL2 OR AR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxId=9606;

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA MEDLINE=99403103; PubMed=10473614;
RA Kim I., Moon S.-O., Koh K.N., Kim H., Uhm C.-S., Kwak H.J., Kim N.-G.,
RA Koh G.Y.;
RT "Molecular cloning, expression, and characterization of angiotensin-
RT related protein. angiotensin-related protein induces endothelial cell
RT sprouting."
RL J. Biol. Chem. 274:26523-26528(1999).
CC -1- FUNCTION: INDUCES SPROUTING IN ENDOTHELIAL CELLS THROUGH AN
CC AUTOCRINE AND PARACRINE ACTION.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEART, SMALL INTESTINE,
CC SPLEEN AND STOMACH. ALSO FOUND IN LOWER LEVELS IN COLON, OVARY,
CC ADRENAL GLAND, SKELETAL MUSCLE AND IN PROSTATE.
CC -1- PTM: N-GLYCOSYLATED.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF125175; AAD53537.1; -.
DR HSSP; P02671; 1FZD.
DR GeneW; HGNC:490; ANGPTL2.
DR MIM: 605001; -.
DR InterPro: IPR002181; fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Signal; Coiled coil; Glycoprotein.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 483 ANGIOPOIETIN-RELATED PROTEIN 2.
FT DOMAIN 76 115 COILED COIL (POTENTIAL).
FT DOMAIN 152 206 COILED COIL (POTENTIAL).
FT DOMAIN 438 450 FIBRINOGEN C-TERMINAL.
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 493 AA; 57104 MW; 0F2ADEE35D185CA CRC64;

Query Match 20.0%; Score 400; DB 1; Length 493;
Best Local Similarity 31.9%; Pred. No. 1.5e-24;
Matches 94; Conservative 50; Mismatches 93; Indels 58; Gaps 11;

QY 97 NELMNRVLLTTEVFKQ-----LDPEPHRPVOSHGLDCTDIKDTIGSVTKTPSG----- 146
DB 231 NRIINOI--STNEIQSDNMLKVLPPPLPTMPPTLT-----SLPSTDKRSGPWRDC 278
QY 147 ----LYIHPEGSSYFEYWCMDYRGGWTVYQKRIGIDFQRLMCDYLD 194
DB 279 LQALEDHGHTSITLYKPEPNTNRLMQWCDOHRDPGCVTYQKRIDGSVNFRRMVEYTKQ 338
QY 195 GFEGDLLGEFWLGLKKEIYIVNOKNTSEMLYVALESEDDTLAASVDNFWLEDETRFEKMH 254
DB 339 GFEGNIDGEYWLGLENIYWLNGN--YKLLVTMEDWSGRKVFAYASFLPESEYKYKRL 396
QY 255 LGRYSGNAGDAFRGLKEDNONAMPSTSDVDNDCGRPACLVNCGSVKSCSHLNKKGW 314
DB 397 LGRYHGNAGDSFTW-----HNGKQFTTLDRDHD-----VYTG-----NCAH-YQKGGW 439
QY 315 FVNCGLANLINGIHFSGLLA---TGIONGTWTKNNSPVKIKSVSMKRIRMPY 366
DB 440 YNACASHNLEWYRGGHYSRYODGVYMAEF--RGGSYSILKVVYMMIRPNPTF 492

RESULT 6
FGL1_HUMAN
ID FGL1_HUMAN STANDARD; PRT; 312 AA.
AC 09UK09;
DT 16-OCT-2001 (rel. 40; Created)
DT 16-OCT-2001 (rel. 40; Last sequence update)
DT 15-JUN-2002 (rel. 41; Last annotation update)
DE Angiopoietin-related protein 2 precursor (Angiopoietin-like 2).
GN ANGPTL2 OR AR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxId=9606;


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DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C.1.
DR SMART: SM00186; FBG.1.
DR PROSITE: PS00514; FIBRIN-AG_C-DOMAIN; 1.
KW Glycoprotein; Coiled coil; Signal; Polymorphism.
FT SIGNAL 1 15
FT CHAIN 16 498
FT DOMAIN 81 119
FT DOMAIN 153 261
FT DOMAIN 284 498
FT CARBOHYD 92 92
FT CARBOHYD 122 122
FT CARBOHYD 154 154
FT CARBOHYD 243 243
FT CARBOHYD 295 295
FT VARIANT 269
FT MISSING (IN CELL LINE T98G; MAY BE DUE TO EXON SLIPPAGE).
FT /FTID-VAR 009940.
SQ SEQUENCE 498 AA; 57513 MW; 5D5FA63AEF6BE920 CRC64;

Query Match 19.8%; Score 395; DB 1; Length 498;
Best Local Similarity 27.0%; Pred. No. 3,9e-24;
Matches 116; Conservative 66; Mismatches 126; Indels 122; Gaps 16;

OY 3 VQNCVYHSTDSVNIIVEDGSNAKDESKNDYCKEDCESDVKTKITREKHFRCRN 62
DB 115 IQONNAVQNHNT---ATMLEIGTSLSTQ-----AEQTRKLDVETQVNLQNSRLIEQL 163
OY 63 LONSIVSY-----TSTFKLLRNMM 82
DB 164 LENSLSYKLEKQLLOQTNEILKIHENKSLLEKHKLEMECKHKEEDLTKEEKENLQGLV 223
OY 83 DEQOASLDYLSNOVN-----ELM---NRVLLLTTEVF-----RKOLDPF 118
DB 224 TRQTYIIQELKELKQSRATNNNSYLQKQLEIMQTVNHLVSLCTKEGVLLGKRKEEKEPF 283
OY 119 PRRPVQSHGLDCTDIKDITGTSVTKTPSGLYTIHPREGSSYFEVWCDMDYRGGWTVYQKR 178
DB 284 -----RDCADVY-----QAGFNKSGIYTIYINNPERKKEVFCNMDVVGCGWTVYQHR 330
OY 179 IDGIIDFORLMCDYLDGFGDLGEFWLGLKIKIFYVNOKRTSMFLYVALESEDDTLAYAS 238
DB 331 EDSGLDFQKGMKRYKMGFGPSEYWLGNFEIFAITSQR--QYMLRLIEMDMEGNRAYSQ 388
OY 239 YDNFWLEDETREFKMLHGRYSNAGDAFRGLKEDN--QNAPEFSTSDVNDGCRPAC-- 294
DB 389 YRFHIGNKEKQNYRLYLKHTGTAG-----KQSSLLHGADEFSTKDADNDQCMCKCAL 441
OY 295 LVNGQSVKSCSHLANKTGMWFNFCGLANLNGIHNF-----GKLATGIGMGCTWTKNNSPV 350
DB 442 MLTG-----GWMFDAQPSNLMNGMYTAGQNHGKL--NGIKWHYF--KGPSY 484
OY 351 KIKSVSMKIR 360
DB 485 SLRSTTMIR 494

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RA Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,
RA Ryan T.E., Bruno J., Radziejewski C., Maissonpierre P.C.,
RA Yancopoulos G.D.;
RT *Isolation of angiotensin-1, a ligand for the TIE2 receptor, by
RT secretion-trap expression cloning.
RL Cell 87:1161-1169(1996).
CC -FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS
CC TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
CC PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
CC CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
CC ENDOTHELIAL AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
CC VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
CC HEART EARLY DEVELOPMENT.
CC -SUBCELLULAR LOCATION: Secreted.
CC -DEVELOPMENTAL STAGE: EARLY IN DEVELOPMENT, AT E9 TO E11, IT IS
CC FOUND MOST PROMINENTLY IN THE HEART MYOCARDIUM SURROUNDING THE
CC ENDOCARDIUM. LATER, IT BECOMES MORE WIDELY DISTRIBUTED. MOST OFTEN
CC IN THE MESENCHYME SURROUNDING DEVELOPING VESSELS. IN CLOSE
CC ASSOCIATION WITH ENDOTHELIAL CELLS.
CC -SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U83509; AAB50558.1; -.
CC HSP; P02671; IFLD.
CC MGI: MGI:108448; Agpt.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C.1.
DR SMART: SM00186; FBG.1.
DR PROSITE: PS00514; FIBRIN-AG_C-DOMAIN; 1.
KW Glycoprotein; Coiled coil; Signal.
FT SIGNAL 1 19
FT CHAIN 20 498
FT DOMAIN 81 119
FT DOMAIN 153 261
FT DOMAIN 284 498
FT CARBOHYD 92 92
FT CARBOHYD 122 122
FT CARBOHYD 154 154
FT CARBOHYD 243 243
FT CARBOHYD 295 295
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 498 AA; 57505 MW; 285B4FDEC26D800 CRC64;

Query Match 19.6%; Score 391; DB 1; Length 498;
Best Local Similarity 26.7%; Pred. No. 8,2e-24;
Matches 115; Conservative 67; Mismatches 126; Indels 122; Gaps 16;

OY 3 VQNCVYHSTDSVNIIVEDGSNAKDESKNDYCKEDCESDVKTKITREKHFRCRN 62
DB 115 IQONNAVQNHNT---ATMLEIGTSLSTQ-----AEQTRKLDVETQVNLQNSRLIEQL 163
OY 63 LONSIVSY-----TSTFKLLRNMM 82
DB 164 LENSLSYKLEKQLLOQTNEILKIHENKSLLEKHKLEMECKHKEEDLTKEEKENLQGLV 223
OY 83 DEQOASLDYLSNOVN-----ELM---NRVLLLTTEVF-----RKOLDPF 118
DB 224 SRQTYIIQELKELKQSRATNNNSYLQKQLEIMQTVNHLVSLCTKEGVLLGKRKEEKEPF 283
OY 119 PRRPVQSHGLDCTDIKDITGTSVTKTPSGLYTIHPREGSSYFEVWCDMDYRGGWTVYQKR 178
DB 284 -----RDCADVY-----QAGFNKSGIYTIYINNPERKKEVFCNMDVVGCGWTVYQHR 330
OY 179 IDGIIDFORLMCDYLDGFGDLGEFWLGLKIKIFYVNOKRTSMFLYVALESEDDTLAYAS 238
DB 331 EDSGLDFQKGMKRYKMGFGPSEYWLGNFEIFAITSQR--QYMLRLIEMDMEGNRAYSQ 388

```

OY 239 YDNFWLEDETRFKMHLGRYSNGNDAFRGLKEDN--QNMFPSTSDVNDGCRPAC-- 294
DB 389 YDRFHIGEKONRYLKGHTAG-----KOSLLHGADFTKADNCKCKAL 441
OY 295 LVNGQSVKSCSHLNKGTGMFNECGLANJNGIHRS---GKLTATGIOMGTWTNNSPV 350
DB 442 MLTG-----GWMFDAGSPSNLNGMYFYAGNHNGL--NGIKMHYF--KGPSY 484
OY 351 KIKSVSKIR 360
DB 485 SLRSTTMMIR 494
RESULT 10
AGP2_HUMAN STANDARD; PRT; 496 AA.
ID AGP2_HUMAN
AC 015123; O9NRR7;
DT 16-OCT-2001 (Rel. 40, last sequence update)
DT 16-OCT-2001 (Rel. 40, last sequence update)
DE Angiopoietin-2 precursor (ANG-2).
GN ANGPT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Lung;
RX MEDLINE=97349327; PubMed=9204896;
RA Mespliere P.C., Suri C., Jones P.F., Bartunkova S., Wiegand S.J.,
RA Radzilewski C., Compton D., McClain J., Aldrich T.H.,
RA Papadopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.;
RT "Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
RT angiogenesis."; Science 277:55-60(1997).
RL [2]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Umbilical vein endothelial cells;
RX MEDLINE=20309815; PubMed=10766762;
RA Kim I., Kim J.-H., Ryu Y.S., Jung S.H., Nah J.J., Koh G.Y.;
RT "Characterization and expression of a novel alternatively spliced
RT human angiopoietin-2."; J. Biol. Chem. 275:18550-18556(2000).
RL [1]
CC -1- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
CC MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY
CC BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH
CC AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY
CC INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR
CC REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL
CC CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
CC ANGIOGENIC SIGNAL.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: 1 (shown here) and 2; are
CC produced by alternative splicing.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF004327; AAB63190.1; -
DR EMBL: AF187858; AAF76526.1; -
DR HSSP: P02671.1; IZFD.
DR Genew: HGNC:485; ANGPT2.
DR MIM: 601922; -
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C; 1.
DR SMART: SM00186; FBG; 1.

DR PROSITE: PS00514; FIBRINAG_C_DOMAIN; 1.
KM Signal: 16
FT CHAIN 17 496
FT DOMAIN 130 256
FT DOMAIN 280 496
FT CARBOHD 89 89
FT CARBOHD 119 119
FT CARBOHD 133 133
FT CARBOHD 151 151
FT CARBOHD 240 240
FT CARBOHD 304 304
FT VARSPLIC 97 148
SQ SEQUENCE 496 AA; 56919 MW; 5642A5847A7385C CRC64;
Query Match 19.1%; Score 381.5; DB 1; Length 496;
Best Local Similarity 26.3%; Pred. No. 4.7e-23;
Matches 110; Conservative 73; Mismatches 138; Indels 97; Gaps 16;
OY 3 VQNCVHHSTDSVVNIYEDGSNARDESKSNDYCKEDCEESCDVYKTI---TREE--- 55
DB 112 IQQNAVONOT---AVMEIGTNLNTQ-----AEGTRKLTVEAGVLANQTRLEQL 160
OY 56 -KHFCRN-LQNSIYSYRSTKLL-----LRNMDEQASL 89
DB 161 LEHSLSTNKLKQLIDQYSEINKLQDKNSFLKVKVLAEMDKHIIQLQSTKEEKDQLQVLY 220
OY 90 DYLSQVNELMNRVLLLT--TEVFRKQ-----LDPPHPVQSH 126
DB 221 SKQNSIIIELEKKIYATVYNNVLOKQOHDMEYNNLLTMSTNSAKDPVAKEDQIS 280
OY 127 GIDCTDIDKTIQSVKTPSGLIYIHPEGSSYFEVWCMDYRGGMVYIQKRIDIQ 186
DB 281 FPDCAEVRKS---GHTNGIYTLTFPNSTEIRKAYCDMEAGCGWTLTIQRREDSVDFQ 336
OY 187 RLMCYLDGFGDLGEPFMGLKIKFIYVQKNTSMVLALESEDDTLAYADFWLEED 246
DB 337 RIKWEYKVGFGSPSEYVGNFVSQLTNQQR--VYLKHLMDWGMENYSLEYHFYLS 394
OY 247 ETRFFKMLHGRYSNGNDAFRGLKEDNQNAMPFSTSDVNDGCRPACLVNGQSVKSCSH 306
DB 395 EELANRIRHLKGLTGRNKR-----SSISQPNDFSTKQDNCK-----ICKSQ 439
OY 307 LHNKGTGMFNECGLANJNGIH---FSGKLTATGIOMGTWTNNSPVKKSVSKIR 360
DB 440 MLT-GWMFDAGSPSNLNGMYFYQRONTKF--NGIKMYW--KSGYSIKATYMMIR 492
RESULT 11
FIBR_HUMAN STANDARD; PRT; 491 AA.
ID FIBR_HUMAN
AC P02675;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
GN FGB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91344740; PubMed=2102623;
RA Chung D.W., Harris J.E., Davie E.W.;
RT "Nucleotide sequences of the three genes coding for human
RL fibrinogen."; Adv. Exp. Med. Biol. 281:39-48(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83283433; PubMed=6688356;
RA Chung D.W., Que B.G., Rixon M.W., Mace M.Jr., Davie E.W.;
RT "Characterization of complementary deoxyribonucleic acid and genomic

RT deoxyribonucleic acid for the beta chain of human fibrinogen.";
 RL Biochemistry 22:3244-3250(1983).
 [13]
 RP SEQUENCE FROM N.A.
 RA Chung D.W., Harris J.E., Davie E.W.;
 RT "Nucleotide sequences of the three genes coding for human
 RL fibrinogen.";
 RL (in) Liu C.Y., Chien S. (eds.);
 RL Fibrinogen, thrombosis, coagulation and fibrinolysis, pp.39-48,
 RL Plenum Press, New York (1991).
 [14]
 RP SEQUENCE FROM N.A., AND VARIANTS SRR-100; HIS-170; LEU-265 AND
 RP LYS-478.
 RA Riederer M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RA Nickerson D.A.;
 RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 [15]
 RP SEQUENCE OF 31-491, AND CARBOHYDRATE-LINKAGE SITE.
 RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
 RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
 RL structural variants.";
 RL (in) Peeters H. (eds.);
 RL Profiles of the biological fluids, Proc. 28th colloquium, pp.51-56,
 RL Pergamon Press, Oxford (1980).
 [16]
 RP SEQUENCE OF 31-491.
 RX MEDLINE-79124640; Pubmed-420779;
 RA Watt K.W.K., Takagi T., Doolittle R.F.;
 RT "Amino acid sequence of the beta chain of human fibrinogen.";
 RL Biochemistry 18:68-76(1979).
 [17]
 RP SEQUENCE OF 31-148, AND DISULFIDE BONDS.
 RX MEDLINE-76225080; Pubmed-936108;
 RA Blomback B., Hessel B., Hogg D.;
 RT "Disulfide bridges in NH₂-terminal part of human fibrinogen.";
 RL Thromb. Res. 8:639-658(1976).
 [18]
 RP SEQUENCE OF 1-38 FROM N.A.
 RX MEDLINE-87146483; Pubmed-3029722;
 RA Huber P., Dalmont J., Courtois G., Laurent M., Assouline Z.,
 RA Marguerie G.;
 RT "Characterization of the 5'-flanking region for the human fibrinogen
 RL beta gene.";
 RL Nucleic Acids Res. 15:1615-1625(1987).
 [19]
 RP SEQUENCE OF 31-44.
 RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
 RT "Studies on fibrinopeptides from primates.";
 RL Acta Chem. Scand. 19:1788-1789(1965).
 [110]
 RP REVIEW, AND DISULFIDE BONDS.
 RX MEDLINE-83254370; Pubmed-6575689;
 RA Henschen A., Lottspeich F., Kehl M., Southan C.;
 RT "Covalent structure of fibrinogen.";
 RL Ann. N.Y. Acad. Sci. 408:28-43(1983).
 [111]
 RP DISULFIDE BONDS.
 RX MEDLINE-77245999; Pubmed-891553;
 RA Gaardlund B., Hessel B., Marguerie G., Murano G., Blomback B.;
 RT "Primary structure of human fibrinogen. Characterization of
 RL disulfide-containing cyanogen-bromide fragments.";
 RL Eur. J. Biochem. 77:595-610(1977).
 [112]
 RP DISULFIDE BONDS.
 RA Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cottrell B.A.,
 RA Cassman K.G., Goldbaum D.M., Doolittle L.R., Friesner S.J.;
 RT "The structures of fibrinogen and fibrin.";
 RL (in) Magnusson S., Ottesen M., Foltmann B., Dano K.,
 RL Neureath H. (eds.);
 RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172,
 RL Pergamon Press, New York (1978).
 [113]
 RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.

RX MEDLINE-84305751; Pubmed-6383194;
 RA Doolittle R.F.;
 RT "Fibrinogen and fibrin.";
 RL Annu. Rev. Biochem. 53:195-229(1984).
 [114]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 164-491.
 RX MEDLINE-97472408; Pubmed-933323;
 RA Spraggon G., Everse S.J., Doolittle R.F.;
 RT "Crystal structures of fragment D from human fibrinogen and its
 RL crosslinked counterpart from fibrin.";
 RL Nature 389:455-462(1997).
 [115]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 164-491.
 RX MEDLINE-98292395; Pubmed-9628725;
 RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
 RT "Crystal structure of fragment double-D from human fibrin with two
 RL different bound ligands.";
 RL Biochemistry 37:8637-8642(1998).
 [116]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE-99175089; Pubmed-10074346;
 RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
 RT "Conformational changes in fragments D and double-D from human
 RL fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
 RL Biochemistry 38:2941-2946(1999).
 [117]
 RP VARIANT BALTIMORE-2.
 RX MEDLINE-89058942; Pubmed-3194892;
 RA Schmeizel C.H., Ebert R.F., Bell W.R.;
 RT "A polymorphism at B beta 448 of fibrinogen identified during
 RL structural studies of fibrinogen Baltimore II.";
 RL Thromb. Res. 52:173-177(1988).
 [118]
 RP VARIANT ISE.
 RX MEDLINE-91208409; Pubmed-2018836;
 RA Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yamazumi K.,
 RA Asakura S., Shirakawa S.;
 RT "A new congenital abnormal fibrinogen Ise characterized by the
 RL replacement of B beta glycine-15 by cysteine.";
 RL Blood 77:1958-1963(1991).
 [119]
 RP VARIANT NAPLES.
 RX MEDLINE-92340664; Pubmed-1634610;
 RA Koopman J., Haverkate F., Lord S.T., Grimbergen J., Mannucci P.M.;
 RT "Molecular basis of fibrinogen Naples associated with defective
 RL thrombin binding and thrombophilia. Homozygous substitution of B beta
 RL 68 Ala->Phe.";
 RL J. Clin. Invest. 90:238-244(1992).
 [120]
 RP VARIANTS JUMUIDEN AND NIJMEGEN.
 RX MEDLINE-92228809; Pubmed-1565641;
 RA Koopman J., Haverkate F., Grimbergen J., Engesser L., Noyakova I.,
 RA Kerst A.F.J.A., Lord S.T.;
 RT "Abnormal fibrinogens Jumuiden (B beta Arg14->Cys) and Nijmegen (B
 RL beta Arg44->Cys) form disulfide-linked fibrinogen-albumin
 RL complexes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:3478-3482(1992).
 [121]
 RP VARIANT NEW YORK-1.
 RX MEDLINE-85157605; Pubmed-3156856;
 RA Liu C.Y., Koehn J.A., Morgan F.J.;
 RT "Characterization of fibrinogen New York 1. A dysfunctional
 RL fibrinogen with a deletion of B beta(9-72) corresponding exactly to
 RL exon 2 of the gene.";
 RL J. Biol. Chem. 260:4390-4396(1985).
 [122]
 RP -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL NODULE.
 CC DIVERGING FROM THIS NODULE ARE 2 THREE-CHAIN COILED COILS, WHICH
 CC CONNECT THE CENTRAL NODULE TO THE DISTAL NODULES CONTAINING THE

DB 46 STKLEKQIIDPOTSEIKLADKNSFLEKKVLDMEKHIVOLRSIKKEKQLOLVKSKONS 105
QY 67 IYASYSR---TKKLNRMDQOASLDYLSNOVNEIMNR-----VLLTTE--VFRKOLD 116
DB 106 IIELEKQIATVATVNNSVYKQOHDMEYVNNMLTLMSTNPSYSLAKKEQIIFR----- 161
QY 117 PFPHRPVOSHGLDCTDIKDTIGSVTK---TPSGLYIHPGSSYPRFVWCDMDYRGCGWT 173
DB 162 -----DC-----GEAFKSGLTSSGYVTLTFPNSYEEIKAYCDMETGCGGWT 202
QY 174 VIOKRIDGIDFQRLMCDYLDGFGDLLGEFWLGLKRIEYVNOKNISFMYALLESDDT 233
DB 203 VIOKRREGSVDFQRYMKEVYFGNPSGEMWLGNEFVSQVTGQR--YVLIKILRDWEGN 260
QY 234 LAYASVDNFWLEDETRFEFKMHLGRYSGNAGDAFRGLKEDNQNAMPSTSDVDNDGCRPA 293
DB 261 EAVSYLDHFYLSNMEILNRYHLKGLGTAKI-----SSISQPGNDSTADADKDC--- 312
QY 294 CLVNGSVKSCSHLHNTKGMWPNDCGLANINGIHH-----PSGKLLATGICMGWTKNNSP 349
DB 313 -----ICKSQMLT--GGMWFDACGSPNINMGYTPQKNTNKF--NGIKWYV--KSG 360
QY 350 VKIKSVSMKIR 360
DB 361 YSLKATTMIR 371

RESULT 13
AGP2_MOUSE
ID AGP2_MOUSE STANDARD; PRT; 496 AA.
AC 035608;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, last sequence update)
DT 16-OCT-2001 (Rel. 40, last annotation update)
DE Angiopoietin-2 precursor (ANG-2).
GN ANGPT2 OR AGPT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=uterus;
MEDLINE=97349327; PubMed=9204896;
RA Maisonneuve P.C., Suri C., Jones P.F., Bartunkova S., Wiegand S.J.,
Radziejewski C., Compton D.L., McClain J., Aldrich T.H.,
Papadopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.,
*Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
angiogenesis.*
RL Science 277:55-60(1997).
CC -1- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY
BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDICERS, SUCH
AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY
INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR
REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL
CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
ANGIOGENIC SIGNAL.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY AT SITES OF VASCULAR
REMODELING.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
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or send an email to license@isb-sib.ch).
CC EMBL: AF004326; AAB63189.1; -.
DR HSSP: P02671; 1FZD.

DR MGD; MG1:1202890; Agpt2.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C; 1.
DR SMART: SM00186; FBG; 1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Glycoprotein; Coiled coil; Signal.
FT SIGNAL 1
FT CHAIN 19
FT DOMAIN 159 256
FT DOMAIN 280 496
FT CARBOHYD 89 89
FT CARBOHYD 119 119
FT CARBOHYD 133 133
FT CARBOHYD 151 151
FT CARBOHYD 240 240
FT CARBOHYD 304 304
SQ SEQUENCE 496 AA; 56616 MW; FA3021FE4E01C410 CRC64;

Query Match 18.7%; Score 374.5; DB 1; Length 496;
Best Local Similarity 25.5%; Pred. No. 1.7e-22;
Matches 110; Conservative 72; Mismatches 125; Indels 125; Gaps 16;

QY 3 VQGNVHSTDSVYNNIVEDGSNAKDESKNDYCKEDESCQYKRTIRFENHFCRN 62
DB 112 IQQNVVQNOT---AVMIEIGTSLNQTAA-----QTRKLTVEAQVNLQTRLEQL 160
QY 63 LQNSIVSYTRSTKRLNRMDQOASLDYLSNOVNEIMNRVLLTTEVF----- 111
DB 161 LQHSI-----STNKLKQIIDQ-----TSEINKLQNKSTFLEQVLDMEGRHSEQL 207
QY 112 -----RKQ---LDPPHPRV-----OSHGLDCTDIKDTIGSVTK-- 142
DB 208 SMKQKDELQVLYVKSQSVIDELEKILVATVNNSLQKQH-----DLMTVNSLLTMM 262
QY 143 -----TPSGLYIHPGSSYPRFVWCDMDYRGCGW 172
DB 263 SSPNSKSVALKRBEQOTFRDCAEIFKSGLTSGIYTLTFPNSYEEIKAYCDMDYVGGGW 322
QY 173 VIOKRIDGIDFQRLMCDYLDGFGDLLGEFWLGLKRIEYVNOKNISFMYALLESDD 232
DB 323 TVIOHREDGSVDFOYRTMKEVYFGNPSGEMWLGNEFVSQVTGQR--YVLIKILKDMEG 380
QY 233 TLAYASVDNFWLEDETRFEFKMHLGRYSGNAGDAFRGLKEDNQNAMPSTSDVDNDGCRP 292
DB 381 NEASLYDHFYLAGESNYRIHLTGLGTAKI-----SSISQGPSFSTDSNDKC-- 433
QY 293 ACLVNGSVKSCSHLHNTKGMWPNDCGLANINGIHH-----PSGKLLATGICMGWTKNNS 348
DB 434 -----ICKSQMLS--GGMWFDACGSPNINMGYTPQKNTNKF--NGIKWYV--KGS 480
QY 349 PVKIKSVSMKIR 360
DB 481 GYSLKATTMIR 492

RESULT 14
FIBR_RAT
ID FIBR_RAT STANDARD; PRT; 479 AA.
AC P14480;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-OCT-1996 (Rel. 34, last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE Fibrinogen beta chain precursor (Contains: Fibrinopeptide B).
GN FGB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=95143386; PubMed=7841303;
RA Courtney M.A., Bunce L.A., Neroni L.A., Simpson-Haldaris P.J.;

RT "Cloning of the complete coding sequence of rat fibrinogen B beta
RT chain cDNA: interspecies conservation of fibrin beta 15-42 primary
RT structure.";
RL Blood Coagul. Fibrinolysis 5:487-496(1994).
RP
RP SEQUENCE OF 1-26 FROM N.A.
RX MEDLINE=84194000; PubMed=6232608;
RA Fowles D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;
RT "Potential basis for regulation of the coordinately expressed
RT fibrinogen genes: homology in the 5' flanking regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).
RN
RN SEQUENCE OF 19-32.
RA Blomback B., Blomback M., Gronlund N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
RN
RN SEQUENCE OF 183-479 FROM N.A.
RX MEDLINE=89378771; PubMed=2673932;
RA Eastman E.M., Galula N.B.;
RT "Cloning and characterization of a cDNA for the B beta chain of rat
RT fibrinogen: evolutionary conservation of translated and
RT 3'-untranslated sequences.";
RL Gene 79:151-158(1989).
RN
RN SEQUENCE OF 425-479 FROM N.A.
RC STRAIN=Wistar; Tissue=Liver;
RX MEDLINE=87134033; PubMed=3817019;
RA Sockak J., Lotli A.-M., Faroux P., Duguet M.;
RT "Molecular cloning of mRNA sequences transiently induced during rat
RT liver regeneration.";
RL Exp. Cell Res. 169:47-56(1987).
CC
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC
CC
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CC or send an email to license@sib-sib.ch).
CC
CC
CC EMBL: U05675; AAA64866.1; -
DR EMBL: M27220; AAA41160.1; -
DR EMBL: K01336; AAA98625.1; -
DR EMBL: M35602; AAA41159.1; -
DR PIR: A05299; A05299.
DR PIR: PE0010; PE0010.
DR HSSP: P02675; 1E2E.
DR InterPro: IPR002181; Fibrinogen.C.
DR Pfam: PF00147; fibrinogen.C; 1.
DR SMART: SM00186; FBG; 1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Blood coagulation; Plasma; Glycoprotein; Signal.
FT SIGNAL 1 18
FT CHAIN 19 479 FIBRINOGEN BETA CHAIN.
FT PEPTIDE 19 32 FIBRINOPEPTIDE B.
FT DISULFID 211 211 INTERCHAIN (WITH THE ALPHA CHAIN)
FT DISULFID 215 215 INTERCHAIN (WITH THE GAMMA CHAIN)
FT DISULFID 219 304 (BY SIMILARITY).
FT DISULFID 229 258 (BY SIMILARITY).
FT DISULFID 412 425 (BY SIMILARITY).

FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 28 30 LSI -> ILS (IN REF. 3).
FT CONFLICT 439 439 L -> O (IN REF. 5).
FT CONFLICT 441 441 S -> T (IN REF. 5).
FT CONFLICT 444 445 S -> A (IN REF. 5).
FT CONFLICT 445 445 R -> K (IN REF. 5).
FT CONFLICT 467 467 V -> F (IN REF. 5).
FT CONFLICT 475 475
SQ SEQUENCE 479 AA; 54303 MW; EC8C6DB77C3BEBC0 CRC64;

Query Match 18.7%; Score 373.5; DB 1; Length 479;
Best Local Similarity 27.2%; Pred. No. 1.9e-22;
Matches 119; Conservative 49; Mismatches 149; Indels 121; Gaps 15;

QY 5 GNCVHNSTSSVNVITVEDSSNKNKDESKSNDYCKEDCEESGVKRTITEEKHFMRNQ 64
DB 81 GGCYHODGDMVL-----CATGCELRQTLNHE-----RP1K 112
QY 65 NSIV-----SYTRSTKLLRNMDQOASLDYLSNOVE----- 98
DB 113 NSIAELNSINSVYESSVTFQYLTLTKDMKKKQAVQNDENVINYSIIDQKLYTD 172
QY 99 -----LMNRVLLTTEVFRKQLD-----PPRPVQSH-----GLDCIDI 133
DB 173 ETVNDNIPRLNRLVLSIILEDLSRKMKLESDISAQTEYCHTPTVCNIPVYSGKECEI 232
QY 134 KPTISVTKTPSGVITIHPEGSSYPREVCMDDYKGGGFTVQKRDIIDFORLMDCL 193
DB 233 IRRGERT-----SEMYLIQDTSSKPRVYCDMKTENGSGTIVQNDQSGVDFGRWMDPK 288
QY 194 DFGGD-----LLGEFVLGLKIFIVYNKNTSFMLYVALSEDDTLAVASYDN 241
DB 289 KFGNATNEDTKKYCGLGEYWLGDKISQTLRGPTL-LLIEEDMKGKVAHYHG 346
QY 242 FVLEDETRFEKMLHGRYSGNAGDAF---RGLKEDN---ONAMPFSTDVNDGCRPA 293
DB 347 FTVQTEANKYQVSVYKKTACNAGALMEGASQLVGENRTVTHNGEFTYDRDNDG---- 402
QY 294 CLVNGQSVSGHLNKGWMEFNEGGLANLNGHHSGL-----LATIGNGTWRK 345
DB 403 -WYTTDPRKQCSK-EDGGGWMYNRCHANPNRYYWGLYSWMSKHGTDDGVVWMMW-- 458
QY 346 NNSPVKIKSVSMKIRMY 363
DB 459 KGSWYSMRMSMKIRPVF 476

RESULT 15
FIBG_HUMAN
ID FIBG_HUMAN STANDARD: PRJ: 453 AA.
AC P02679; P04469; P04470; Q96KJ3; Q96A14;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen gamma chain precursor (PRO2061).
GN FGG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS GAMMA-A AND GAMMA-B).
RX MEDLINE=85252774; PubMed=2990550;
RA Rixon M.W., Chung D.W., Davie E.W.;
RT "Nucleotide sequence of the gene for the gamma chain of human
RT fibrinogen.";
RL Biochemistry 24:2077-2086(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83283434; PubMed=6688357;
RA Chung D.W., Chan W.-Y., Davie E.W.;
RT "Characterization of a complementary deoxyribonucleic acid coding for
RT the gamma chain of human fibrinogen.";
RL Biochemistry 22:3250-3256(1983).

RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS GAMMA-A AND GAMMA-B).
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi O.,
 RA Nickerson D.A.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM GAMMA-A).
 RC TISSUE-Fetal liver;
 RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M.,
 RA He F.;
 RT "Functional prediction of the coding sequences of 33 new genes deduced
 RT by analysis of cDNA clones from human fetal liver."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM GAMMA-A).
 RC TISSUE-Skeletal muscle;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 27-437.
 RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
 RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
 RT structural variants."
 RL (in) Peeters H. (eds.);
 RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
 RL Pergamon Press, Oxford (1980).
 RN [7]
 RP SEQUENCE OF 75-286 FROM N.A.
 RC TISSUE-liver;
 RA MEDLINE-92119334; PubMed-1685103;
 RA Marchetti L., Zaneli T., Malcovati M., Tencchini M.L.;
 RT "Polymorphism of the human gamma chain fibrinogen gene."
 RL DNA Seq. 1:419-422(1991).
 RN [8]
 RP SEQUENCE OF 285-437 FROM N.A. (ISOFORMS GAMMA-A AND GAMMA-B).
 RA MEDLINE-85030379; PubMed-6092346;
 RA Fornace A.J. Jr., Cummings D.E., Comeau C.M., Kant J.A.,
 RA Crabtree G.R.;
 RT "Structure of the human gamma-fibrinogen gene. Alternate mRNA
 RT splicing near the 3' end of the gene produces gamma A and gamma B
 RT forms of gamma-fibrinogen."
 RL J. Biol. Chem. 259:12826-12830(1984).
 RN [9]
 RP SEQUENCE OF 209-270 FROM N.A.
 RA MEDLINE-84069777; PubMed-6689067;
 RA Inam A.M.A., Eaton M.A.W., Williamson R., Humphries S.;
 RT "Isolation and characterisation of cDNA clones for the A alpha- and
 RT gamma chains of human fibrinogen."
 RL Nucleic Acids Res. 11:7427-7434(1983).
 RN [10]
 RP SEQUENCE OF 411-453 (ISOFORM GAMMA-B).
 RA MEDLINE-82068993; PubMed-7306501;
 RA Wolfenstein-Todel C., Moseson M.W.;
 RT "Carboxy-terminal amino acid sequence of a human fibrinogen
 RT gamma-chain variant (gamma')."
 RL Biochemistry 20:6146-6149(1981).
 RN [11]
 RP REVIEW, AND DISULFIDE BONDS.
 RA Henschen A., Lottspeich F., Kehl M., Southan C.;
 RT "Covalent structure of fibrinogen."
 RL Ann. N.Y. Acad. Sci. 408:28-43(1983).
 RN [12]
 RP DISULFIDE BONDS.
 RA Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cottrell B.A.,
 RA Cassman K.G., Goldbaum D.W., Doolittle L.R., Friesner S.J.;
 RT "The structures of fibrinogen and fibrin."
 RL (in) Magnusson S., Ottesen M., Foltmann B., Dano K.,
 RL Neurath H. (eds.);
 RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172,
 RL Pergamon Press, New York (1978).
 RN [13]
 RP DISULFIDE BONDS.
 RX MEDLINE-76225080; PubMed-936108;
 RA Blomback B., Hessel B., Hogg D.;
 RT "Disulfide bridges in NH2-terminal part of human fibrinogen."
 RL Thromb. Res. 8:639-658(1976).
 RN [14]
 RP QUATERNARY STRUCTURE, AND DISULFIDE BONDS.
 RX MEDLINE-83231465; PubMed-6860649;
 RA Hoepflich P.D., Doolittle R.F.;
 RT "Dimeric half-molecules of human fibrinogen are joined through
 RT disulfide bonds in an antiparallel orientation."
 RL Biochemistry 22:2049-2055(1983).
 RN [15]
 RP SULFATION.
 RX MEDLINE-91369960; PubMed-1892842;
 RA Farrell D.H., Mulvihill E.R., Huang S., Chung D.W., Davie E.W.;
 RT "Recombinant human fibrinogen and sulfation of the gamma' chain."
 RL Biochemistry 30:9414-9420(1991).
 RN [16]
 RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
 RX MEDLINE-84305751; PubMed-6383194;
 RA Doolittle R.F.;
 RT "Fibrinogen and fibrin."
 RL Annu. Rev. Biochem. 53:195-229(1984).
 RN [17]
 RP POLYMERIZATION SITE.
 RX MEDLINE-85014892; PubMed-6592597;
 RA Horwitz B.H., Varadi A., Scheraga H.A.;
 RT "Localization of a fibrin gamma-chain polymerization site within
 RT segment Thr-374 to Glu-396 of human fibrinogen."
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5980-5984(1984).
 RN [18]
 RP POLYMERIZATION SITE.
 RX MEDLINE-81142375; PubMed-6451630;
 RA Oleksa S.A., Budzynski A.Z.;
 RT "Localization of a fibrin polymerization site."
 RL J. Biol. Chem. 256:3544-3549(1981).
 RN [19]
 RP PLATELET AGGREGATION SITE.
 RX MEDLINE-84203545; PubMed-6326808;
 RA Kloczewiak M., Timmons S., Lukas T.J., Hawiger J.;
 RT "Platelet receptor recognition site on human fibrinogen. Synthesis
 RT and structure-function relationship of peptides corresponding to the
 RT carboxy-terminal segment of the gamma chain."
 RL Biochemistry 23:1767-1774(1984).
 RN [20]
 RP PLATELET AGGREGATION SITE.
 RX MEDLINE-84185664; PubMed-6325435;
 RA Plov E.F., Strouj A.H., Meyer D., Marguerie G., Ginsberg M.H.;
 RT "Evidence that three adhesive proteins interact with a common
 RT recognition site on activated platelets."
 RL J. Biol. Chem. 259:5388-5391(1984).
 RN [21]
 RP CALCIUM-BINDING SITE.
 RX MEDLINE-85261382; PubMed-3160702;
 RA Dang C.V., Ebert R.F., Bell W.R.;
 RT "Localization of a fibrinogen calcium binding site between
 RT gamma-subunit positions 311 and 336 by terbium fluorescence."
 RL J. Biol. Chem. 260:9713-9719(1985).
 RN [22]
 RP CHROMATOGRAPHIC COMPARISON OF GAMMA-A AND GAMMA-B CHAINS.
 RX MEDLINE-81054908; PubMed-6933547;
 RA Wolfenstein-Todel C., Moseson M.W.;
 RT "Human plasma fibrinogen heterogeneity: evidence for an extended
 RT carboxyl-terminal sequence in a normal gamma chain variant
 RT (gamma')."
 RL Proc. Natl. Acad. Sci. U.S.A. 77:5069-5073(1980).
 RN [23]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.
 RX MEDLINE-97169449; PubMed-9016719;
 RA Yee V.C., Pratt K.P., Cote H.C.F., le Trong I., Chung D.W.,
 RA Davie E.W., Stenkamp R.E., Teller D.C.;
 RT "Crystal structure of a 30 kDa C-terminal fragment from the gamma
 RT chain of human fibrinogen."

RL Structure 5:125-138(1997).
 RN [24]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.
 RX MEDLINE-97352771; PubMed-9207064;
 RA Pratt K.P., Cote H.C.F., Chung D.W., Stenkamp R.E., Davie E.W.;
 RT "The primary fibrin polymerization pocket: three-dimensional
 RT structure of a 30-kDa C-terminal gamma chain fragment complexed with
 RT the peptide Gly-Pro-Arg-Pro.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:7176-7181(1997).
 RN [25]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 114-432.
 RX MEDLINE-97472408; PubMed-9333233;
 RA Spraggon G., Everse S.J., Doolittle R.F.;
 RT "Crystal structures of fragment D from human fibrinogen and its
 RT crosslinked counterpart from fibrin.";
 RL Nature 389:455-462(1997).
 RN [26]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 114-432.
 RX MEDLINE-98292395; PubMed-9628725;
 RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
 RT "Crystal structure of fragment double-D from human fibrin with two
 RT different bound ligands.";
 RL Biochemistry 37:8637-8642(1998).
 RN [27]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE-99175089; PubMed-10074346;
 RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
 RT "Conformational changes in fragments D and double-D from human
 RT fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
 RT
 Query Match 18.6%; Score 371.5; DB 1; Length 453;
 Best Local Similarity 31.9%; Pred. No. 2,6e-22;
 Matches 105; Conservative 42; Mismatches 129; Indels 53; Gaps 11;
 QY 65 NSIVSTNSTKRLNNMDEQ-----QASLDYLSNQVNELMNRYLLTTEVFRKQLDPF 118
 DB 103 NMIDATILKSRMLEIMKYEASILTHDSIRYLOEIYNSNNQKIYNLKEKY--AQLEAQ 160
 QY 119 PRRP-----VQSH---GLDQTDIKDTIGSVTKTPSGLYITHPEGSSYFEVMCDMDYRGSG 171
 DB 161 COEPCKDVIQHDITGKDCQD---IANKGAKQSGLYFTKPLKANQOFLVCEIDSGGNG 216
 QY 172 WTVIQRIIDGIDFQRLMCDYLDGFGDL---LGEFWLGLKRIFYIVNQKNTSFMLYVAL 227
 DB 217 WTVFQKRLDGSYDFKKNWIQYKEGHLSPGTTEFWLQNEKIHLSIQSAIPYALVEL 276
 QY 228 ESEDDTLAYASTDNFWLEDETFEPFKMHLGRYS-GNAGDAFRLKED-----NQNAM 278
 DB 277 EDWNGRTSTADYAMFKYVGEADKRYRLTYAYFAGGDADAFDFGDDPSDKFTSHNGM 336
 QY 279 PESTSDVDNDGCRPACLVNGQSVKSGSHLANKGMWENECGLANLGIHFGKL----- 333
 DB 337 QPSTWDNDNDKFEQNCADQDS-----GWMNKCCHAGHLNGVYVGGTYSKAST 385
 QY 334 --LATGIQMGWTTRKNSPVKIKSVSMKI 359
 DB 386 PNGYDNGIIMATW--KTRWYSMKKTTMTKI 412

Search completed: December 16, 2002, 17:34:41
 Job time : 10.7619 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 16, 2002, 17:32:08 ; Search time 27.746 Seconds
(Without alignments)
2732.835 Million cell updates/sec

Title: US-09-596-196-9

Perfect score: 2000
Sequence: 1 EVVQNCVHSTDSVYVIV.....PVKIKSVMKIRRMNPFYK 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

- Listing first 45 summaries
- 1: SP_TREMBL_21.*
 - 2: sp_archaea.*
 - 3: sp_bacteria.*
 - 4: sp_fungi.*
 - 5: sp_human.*
 - 6: sp_invertebrate.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phage.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_virus.*
 - 16: sp_bacteriap.*
 - 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	427.5	21.4	652	5	Q9NDQ1	Q9ndq1 ciona intes
2	425	21.2	491	4	O9S841	O9s841 homo sapien
3	409.5	20.5	357	11	O9EPT7	O9ept7 ratcus norv
4	404.5	20.2	493	11	O9J003	O9j003 ratcus norv
5	399.5	19.5	489	13	O9O218	O9o218 brachydanto
6	390	19.0	498	6	O9BDY8	O9bdy8 sus scrofa
7	382	19.1	495	4	O9P2Y7	O9p2y7 homo sapien
8	379.5	19.0	346	4	O43827	O43827 homo sapien
9	379.5	19.0	496	11	O9D2D2	O9d2d2 mus musculu
10	378.5	18.9	407	13	O9DER1	O9der1 gallus gall
11	378.5	18.9	488	13	O91589	O91589 xenopus lae
12	378.5	18.9	493	13	O9DER2	O9der2 gallus gall
13	376.5	18.8	441	13	O9DER0	O9der0 gallus gall
14	375	18.8	308	5	O9UBW6	O9ubw6 tachyples
15	373.5	18.7	496	6	O9BDY7	O9bdy7 sus scrofa
16	370	18.5	316	5	O9UBW7	O9ubw7 tachyples

17	369.5	18.5	220	5	O8T8A2	O8t8a2 ciona savig
18	368.5	18.4	407	13	O9PU54	O9pu54 gallus gall
19	368.5	18.4	436	4	O8WU3	O8wu3 homo sapien
20	368.5	18.4	436	11	O8VCW5	O8vcw5 mus musculu
21	368	18.4	314	11	O8VC25	O8vc25 mus musculu
22	367.5	18.4	337	11	O8RIQ3	O8riq3 mus musculu
23	364.5	18.2	431	6	O951U3	O951u3 macaca fasc
24	364.5	18.2	513	13	O9O219	O9o219 brachydanto
25	359	17.9	244	4	O9HBP3	O9hbp3 homo sapien
26	359	17.9	341	5	O966W1	O966w1 halocynthia
27	358	17.9	435	13	O93568	O93568 gallus gall
28	357.5	17.9	932	13	O57587	O57587 brachydanto
29	354	17.7	356	5	O95P98	O95p98 halocynthia
30	352.5	17.6	592	4	O95697	O95697 homo sapien
31	352.5	17.6	1294	4	O9U0P3	O9u0p3 homo sapien
32	352	17.6	324	5	O95PA0	O95pa0 halocynthia
33	348	17.4	292	5	O9UBW8	O9ubw8 tachyples
34	347	17.3	324	5	O95P99	O95p99 halocynthia
35	341	17.1	316	6	O28529	O28529 mustela put
36	339	17.0	712	4	O00531	O00531 homo sapien
37	339	17.0	1358	4	O92752	O92752 homo sapien
38	339	17.0	1358	4	O15568	O15568 homo sapien
39	333.5	16.7	372	5	O18545	O18545 biomphalari
40	333.5	16.7	385	5	O95U09	O95u09 biomphalari
41	332.5	16.6	337	6	O9BE00	O9be00 macaca fasc
42	330	16.5	1356	11	O05546	O05546 ratcus norv
43	327.5	16.4	235	6	O28763	O28763 papio cynoc
44	327.5	16.4	1353	13	O00546	O00546 gallus gall
45	321.5	16.1	440	5	O9W291	O9w291 drosophila

ALIGNMENTS

RESULT 1

ID	Q9NDQ1	PREDIMINARY;	PRT;	652 AA.
AC	O9NDQ1;			
DT	01-OCT-2000 (TREMBLrel. 15, created)			
DT	01-OCT-2000 (TREMBLrel. 15, last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, last annotation update)			
DE	Fibrinogen-like protein.			
GN	Cl-FIBRN.			
OS	Ciona intestinalis.			
OC	Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;			
OC	Phelebranchia; Clonidae; Ciona.			
OX	NCBI_TaxID=7719;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Hotta K., Takahashi H., Asakura T., Satoh B., Takatori N., Satou Y.,			
RA	Satch N.;			
RT	"Characterization of Brachyury downstream notochord genes in the Ciona			
RT	intestinalis embryo."			
RL	Submitted (Jan-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB036849; BAB00626.1; -.			
DR	HSSP; P02671; IFZD.			
DR	InterPro; IPR002181; Fibrinogen_C.			
DR	Pfam; PF00147; fibrinogen_C; I.			
DR	SMART; SM00186; FBG; I.			
DR	PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.			
DR	PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.			
DR	SEQUENCE 652 AA; 73252 MW; A492BA325162F0E0 CRC64;			

Query Match 21.4%; Score 427.5; DB 5; Length 652;
Best Local Similarity 30.7%; Pred. No. 6.7e-27;
Matches 115; Conservative 67; Mismatches 124; Indels 69; Gaps 16;

QY	30	SKSDNYCK---EDPESCDVTKITREKHEM-----CRNLQSIYSYRS-----	73
DB	293	SOENDDAKEAEEDVTRIVETTDVATGVEQYTTDEDETSTSTSGVTSRDTHENN	352
QY	74	---TKLIRNMMDROQSL-----DYSNOVN--ELMNRVLLLTTEYFRKL	115
DB	353	EMFTSTVTHAVEVTOPIYISSESGSVNIRDGATNETEGIEFTSRILRAT-----	404

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QY 116 DPFHRRPQSGHGL--DCTDIDITIGSVTKRPSGLYIIHPGSSSYPEFVMCDMDYRGGW 173
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Db 405 NPTFVDQGGFTSLSLYDCDAELX----AGVAGQSGYVDIRP-GTKATWYVYUCMDMDGGWT 459
      :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 174 VIOKRIGIIDFQRLKCDYLDGFGDLLGEFNLGJLKTIFY-I-VNOKNTSPMLVYALBESDD 232
      :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 460 MLCRRIDGIVPFSGWMKSYKRGFEDDIADHWIGLEKMHISTSKSRHMLRLINTLTDWDD 519
      :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 233 TLAAASYDNFMLEDETRFEKHNHLGRYSAGNGDAFRGLKTKEDNONAMPEFSVDVNDGCRP 292
      :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 520 VSHRANTGVPIIRBEGKNQYOLLAIRYGTAGDAL-NGCEMYNNHLDPTTFDDND----- 574
      :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 293 ACIVNGQSVKSCSHLHNKTKGWMNEGCLIANLNGIHNESG--KLLANGIOWGTWK----- 345
      :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 575 -----GYALGNCGRYY-RSGWMFNACFAANLNG-NYYTGYKGVQNGIYGTWYKLDST 627
      :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 346 NNSPVKIKTSVSMKTR 360
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Db 628 SNSRYSFYDMKVR 642
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RESULT 2	Q95841	PRELIMINARY;	PTT;	491 AA.
AC	Q95841;			
DT	01-MAY-1999 (TrEMBLrel. 10, Created)			
DT	01-MAY-1999 (TrEMBLrel. 10, Last sequence update)			
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)			
DE	Angiopoletin Y1 (DU595C2.2) (Angiopoletin-related protein 1 precursor).			
GN	DU595C2.2 OR ARP1.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=HEART;			
RA	KIM I., Kwak H.J., Ahn J.E., So J.N., Liu M., Koh K.N., Koh G.Y.;			
RT	"Molecular cloning and characterization of a novel angiopoietin family protein, angiopoietin3."			
RL	FEBS Lett. 443:353-356(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Cobley V.;			
RT	Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.			
RL	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=PLACENTA;			
RA	Ota T., Nishikawa T., Kawai Y., Suzuki Y., Ishii S., Salto K., Yamamoto J., Sugano S., Isogai T.;			
RT	"hRI human cDNA sequencing project."			
RL	Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=PLACENTA;			
RA	Ito Y., Oike Y., Yasunaga K., Matsumoto S., Ota T., Nishikawa T., Kawai Y., Isogai T., Hamada K., Saito Y., Miyata K., Masuho Y., Suda T.;			
RT	"Molecular cloning and characterization of novel angiopoietin-related protein (ARP4)."			
RL	Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.			
DR	EMBL: AF107253; AND19608.1; -			
DR	EMBL: AL355520; CAC13169.1; -			
DR	EMBL: AB056476; BAB40691.1; -			
DR	HSSP: P02671; 1FZD.			
DR	InterPro: IPR002181; Fibroinogen-C.			
DR	Pfam: PF000147; fibroinogen_C.1.			
DR	SMART: SM00186; FBG; 1.			
DR	PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.			
DR	Signal.			

FT	SIGNAL	1	23	POTENTIAL.
FT	CHAIN	24	491	POTENTIAL.
SEQ	SEQUENCE	491 AA;	56719 MM;	3C4DBDDE6CF7E99 CAC64;
	Query Match		21.2%;	Score 425; DB 4; Length 491;
	Best Local Similarity		26.9%;	Pred. No. 7.4e-27;
	Matches 119;		Conservative 64;	Mismatches 133; Indels 126; Gaps 14;
OY	24	SNARESSNDPYVCKEDDEESCDVATKTRT-EKHFMCRNLONSIVSTRSKLLRRNM	82	
Db	68	TKGQASITKMDITRDELENLKDVLSRKRREIDVLQVLVDGNIYNEVKYLKRKESRNM	127	
OY	83	DE-QDASIDYL-----SQNVELMNRVLLTTE-----	109	
Db	128	SRVYQLYQMLHEITRKDNLSLESOLEKNIIVNTTEMIKATRRLEVKYASTLDLVN	187	
OY	110	-----VFRKQ--LDP-----FPHRVOSHGL-----	128	
Db	188	NQSVITLLEEQCLIFSRQDTHVSRLVQVVRQIHNPISQVTLRDLGNETQRDPYPR	247	
OY	129	DCTDIKDTIGSYTKRP-----SCLYIHREGSYPREV	161	
Db	248	DLMPRPDLATSPKSPFKIPRYTFINEGPFKDCQOAKKAGHSVSGLYMIKRPENSGMQL	307	
OY	162	MCDMDYRGGGWVYIOKRIDGIIIDPRLMODYLDEGSDLLGEVWELKIKFYIVNOKNTSE	221	
Db	308	WCENSLDRPGWVIOKRTDGSVNEFRMNEVKKGGGIDGEXWLELENTYLSNODN--Y	365	
OY	222	MLYVLESEDDTLAASVDNFWLEDETEFEFKMLRLYSGNAGADAFRGLEKEDNQAMPFS	281	
Db	366	KLLIELEDMOSDKKYAAEYSSFRLEDESEYRIARLDTYQGNAGDSMMW-----HNGKQFT	419	
OY	282	TSDVDNDCGRPACLVNGGSVWSSCHLHNKTKGWPNFEGCLANGIINHFSKLLA--TGI	338	
Db	420	TLDRLKCD-----MYAGNCALFH--KGGWYNAACASHSNLNGWYRGGHYRSKHOGI	468	
OY	339	QMGTFWKNNSPYKIKSVGSKTR	360	
Db	469	FMAET--RGSTSLRAVQPMTR	488	

```

RESULT 3
Q9EPF7
ID Q9EPF7 PRELIMINARY; PRT: 357 AA.
AC Q9EPF7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Prothrombinase FGL2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Rychlik D.F., Chlen E., Philippe M.;
RT "FGL2 Expression in the Sprague-Dawley Rat.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF323608; AAG42269.1; -.
DR HSSP; P02671; 1F2D.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 357 AA; 40966 MW; 31183DD9A02EBBA9 CRC64;

Query Match 20.5%; Score 409.5; DB 11; Length 357;
Best Local Similarity 32.0%; Pred. No. 9.3e-26;
Matches 121; Conservative 50; Mismatches 150; Indels 57; Gaps 15;

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```
Db 4 VLKEVTLQEAVDLSLKKSCQDCKLQADEHPDPCNGAETAED-----NRQVLESQVKN 57
QY 74 TKLLRNMADEOQA-----SL-----DYLNSQVNELMARVLLLTTEVER----- 112
Db 58 LSELKNAKEEIIQLOGRLLESJLQVMMNNIENTVDKNVANTLTVSNVSLDSKCKPSQEH 117
QY 113 KOLDPPHAPVOSHGLDCDIDIKDTIGSVTKTPSGLYIIHPEGSSYPEVNCMDYRGCGW 172
Db 118 NQNPVQHLIYK-----DCSDYV-VLG---KRSSGTYRVDPDHNNSPREYVCDMETTGGW 169
QY 173 TVYQKRIIDGIDFQRLMCLYDLGFGDLGFEFMGLKIFIVYQKNTSFMLYALSEDD 232
Db 170 TVYQARLDSTNETFRMKYKAGFNLEREFMGLNDKIHLLT--KSKEMILRIDLEDENG 227
QY 233 TLAYASVDNFWLEDETRFFRMHLGRYSGNAGDAFRGLKKEDENONAMPFSTDVNDQCRP 292
Db 228 LTIYAVYDDPFYANEFKLRLHGNNGTRAGDLR-FSRHYNDLRFETTPDDNDNRYPS 286
QY 293 ACLVNGQSVKCSHLNKTGWPFNECGLANLNGIH--FSGRLATGLOMGTW--TRKN 347
Db 287 G-----NCG-LYSSGWFMDACLASNLNGKYNNQRYKG--VRNGIFMGTPGVSOA 334
QY 348 SPYKIKSVSKIRRMNP 365
Db 335 HPGYKFSFKAKMIRP 352
```

RESULT 4

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Q9J303 PRELIMINARY; PRT; 493 AA.
ID 09J303;
AC 09J303;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Angiotensin II type 1A receptor associated protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MISTAR-KYOTO; TISSUE=VASCULAR SMOOTH MUSCLE;
RA Guo D.F., Baranes D., Ono Y., Porter J.P., Adi-Daoude E., Orlov S.N.,
RA Inagami T.;
RT "Arap1 is required for recycling and resensitization of angiotensin II
RT type 1A receptor.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF159043; AAF80364.1; -.
DR HSSP; P02671; 1FZD.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C.1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Receptor.
SQ SEQUENCE 493 AA; 57159 MW; 7C37652C472B2341 CRC64;
```

Query Match 20.2%; Score 404.5; DB 13; Length 493;
Best Local Similarity 27.1%; Pred. No. 3, 7e-25;
Matches 108; Conservative 68; Mismatches 118; Indels 105; Gaps 15;

```
QY 42 EESCDVTKIT-----REEKHMCRLNLSIVSTRSKLLRNMADEOQ--A 87
Db 125 KESRRNMSRVTLQYMLLHEIRKRDNALSELQLENILNOTADMQLVSKYKLEHKFQ 184
QY 88 SLDYLSNQVNEIM-----NRVL--LTTEVER 112
Db 185 HLDMLAHNOSEVIAQLAEHCQRPAPRVQPPRPVRYQRPPTYNRILNQISTNEIOS 244
QY 113 KO-----LDP-FPIHPVOSHGLDCTIDKTIGSVTKTPSG-----LYII 150
Db 245 DQMLKVLFPFLPTMPLT-----SLPSSIDKPSGFWRCQLALLEDGHSSTSYLV 294
QY 151 HPGSSYPFEVNCMDYRGCGWTVIQKRIIDGIDFQRLMCLYDLGFGDLGFEFMGLKRI 210
```

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Db 295 KPEPTNRLMQWCDQDRDPCGWTVIQRRLDGSVNFFNNWETRYKQGFENIGEFYMLGLENI 354
QY 211 FIYVQKNTSFMLYVLAESDDTLAVASYDNFMLEDETRFFKNHILGYSGNAGDAFRGLK 270
Db 355 YMLTNQGN--YKLVLTWEDNSGKRVFAETVASFLEPSEYIKLGLGYHGNAGDSPTW-- 410
QY 271 KEDONAMPFSTSDVDNDGCRPACTLVNGQSVKCSHLNKTGWPFNECGLANLNGIHPS 330
Db 411 -----HNGKQFTTIDRHD-----YITG-----NCAH-YQKGGWVYKCAHSLNGLVYRG 455
QY 331 GKLLA--TGIOWGTWTKNSPYKIKSVSKIRRMNPY 366
Db 456 GHYRSRYQDGVYMAEF--RCGSYSLKRVVMIRPNPTWF 492
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RESULT 5

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Q90218 PRELIMINARY; PRT; 489 AA.
ID 090218;
AC 090218;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Angiopoietin-2.
GN ANG2.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21391693; PubMed=11500985;
RA Pham V.N., Roman B.L., Weinstein B.M.;
RT "Isolation and expression analysis of three zebrafish angiopoietin
RT genes.";
RL Dev. Dyn. 221:470-474(2001).
DR EMBL; AF379603; AAK83348.1; -.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C.1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; UNKNOWN.1.
SQ SEQUENCE 489 AA; 55785 MW; 3ABAB6278539B33C CRC64;
```

Query Match 20.0%; Score 399.5; DB 13; Length 489;
Best Local Similarity 28.1%; Pred. No. 9, 4e-25;
Matches 114; Conservative 55; Mismatches 131; Indels 105; Gaps 16;

```
QY 3 VQNCVHSHSDSSVNVNIVEDGSSNAKDESKSNDYCKEDCESDVTKITREEKHMCRN 62
Db 107 MERNVHTQ-----ATMLEIGTNLLSQSAEN--TCK-----LTVETQVNLNQTG-----R 150
QY 63 LQNSIVSTRSKLLRNMD-----EQQA 87
Db 151 LEIQLESLSTNRLKOLETOEVSRLDNKSNMYDRFADMAKHSRELQALQOEQQ 210
QY 88 SLDYLSNQVNEIM-----RVLLLTTEVERKQDDPPH-----RPVQS 125
Db 211 LLELLDQ--NELVSVLLLEGELASSTRNSTLIQROQASLTDYQQLLAWHNDISTPYDK 269
QY 126 HGL--DCTDI-KDTIGSVTKTPSGLYIIHPEGSSYPEVNCMDYRGCGWTVIQKRIID 181
Db 270 EMLKFRCAEIEFGSV-----TENGIVSIHLRPNSTOKIKVPCDKMKTGSGGWTVQHRVYDG 324
QY 182 IIDFQRLMCLYDLGFGDLGFEFMGLKIFIVYQKNTSFMLYALSEDDTLAYASVDN 241
Db 325 SVDFNRQWMDYKLGFGDPSGGEHLGNDVYHLLTTPKD--YTLQVLADEHQAQVSDYT 382
QY 242 FWLEDETRFFFMHLGRYSGNAGDAFRGLKKEDENONAMPFSTDVNDQCRPACTLVNGQSV 301
Db 383 FYIDGEDKKYSLHARGSPGTAGRT-----SSLTISGTOFSTKDDNDQC----- 426
QY 302 KCSGHLNKT--GMPFNECGLANLNGIHNF--SGKLATGLOMGTW 343
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Db	427	-SCKQAMATGSMWFEACGSPSLNLTYYSGNBNVIRNSIKRYW	470
RESULT 6			
Q9BDY8			
AC	Q9BDY8	PRELIMINARY:	PRT: 498 AA.
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	Angiopoietin 1.		
OS	Sus scrofa (Pig).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euteria; Cetartiodactyla; Suina; Suidae; Sus.		
OX	NCBI_TaxID:9623;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21153163; PubMed=11230987;		
RA	Kim I., Moon S.O., Han C.Y., Pak Y.K., Moon S.K., Kim J.J., Koh G.Y.;		
RT	"The angiopoietin-like system in coronary artery endothelium prevents		
RT	oxidized low-density lipoprotein-induced apoptosis."		
RL	Cardiovasc. Res. 49:872-881(2001).		
DR	EMBL; AF233227; AAK14992.1; -.		
DR	HSSP: P02671; 1FZD.		
DR	InterPro: IPR002181; Fibrinogen_C.		
DR	Pfam; PF00147; Fibrinogen_C; 1.		
DR	SMART; SM00186; FBG; 1.		
DR	PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.		
DR	SEQUENCE 498 AA; 57413 MW; ABC1CBF56061876 CnC64;		
Query Match	19.5%; Score 390; DB 6; Length 498;		
Best Local Similarity	26.7%; Pred. No. 5.9e-24;		
Matches 115; Conservative 66; Mismatches 127; Indels 122; Gaps 16;			
QY	3 VQGNVHHSTSSVNVIVEDGSNADKESNDTVCKEDQESCDYKTKITREKHFNRN 62		
DB	115 IQQNVQVHNT-----ATMLEIGTSLSTQ-----AEQTRKLTIVETQVLTNSTLETQL 163		
QY	63 LQNSIVSY-----TRSTKLLRNMM 82		
DB	164 LENSLSYTKLEKQLDQTNELIKIHEKNSLLEKILTEMGKKKEELDTLKEKENLQGLV 223		
QY	83 DEQASLDLYLSQNV-----ELM-----NRVLLTTEVF-----RKQLDF 118		
DB	224 TRQTYIYDELKKQLRATTNNSVLQKQLELMDTVHNLVNLCTKGGVLLKGGKKEVPRF 283		
QY	119 PHRVQSHGLDCTDKDTIGSVTKTPSGIYIIRPGSSYPREVMDNDYRGSGWVQKR 178		
DB	284 -----RQCADVY-----QAGFKSSITYYIYINMPKPKVFPNMDLNGSGWTVIYHR 330		
QY	179 IDGLIDFQRLMCDYLDGFGDLLGEFMDLKKIFYLVNOKNTSFMLYVALSEDDTLAAS 238		
DB	331 EDGSLDFPRGMKEYMGKGNPSGEVWLGNFIFATTSQR--QYLTRELMDEGNRAISQ 388		
QY	239 YDNFLEDETEPFKKHLRLYSGNAGDARGLKEDN--QNAPESTSVYDNDGCRPAC-- 294		
DB	389 YDRFIGNKEKNYRLYLGHSGTAG-----KQSLILHAGDFSTKADNDNCMKCAL 441		
QY	295 LVNQGVSVCSHLHKTKGWFMEGGLANTLNGIHHS-----GKLATGQMGWTVTKNNSPV 350		
DB	442 MLTG-----GMWFDACGSPSLNGEFTYAGQNHGKL--NGIKMYF--KGPSY 484		
QY	351 KIKSVSMKIR 360		
DB	485 SLRSTTMIR 494		
RESULT 7			
Q9P2Y7			
AC	Q9P2Y7	PRELIMINARY:	PRT: 495 AA.
DT	01-OCT-2000 (TREMBLrel. 15, Created)		
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		

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DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
OC Angiopoietin-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN
  RP SEQUENCE FROM N.A.
  RM MEDLINE=99126459; PubMed=9927494;
  RA Tanaka S., Mori M., Sakamoto Y., Makuchi M., Sugimachi K.,
  RT "Biologic significance of angiopoietin-2 expression in human
  RL hepatohepatic carcinoma."
  RL J. Clin. Invest. 103:341-345(1999).
  DR EMBL; AB009865; BAA95590.1; -.
  DR HSPB; P02671; IEPD.
  DR InterPro: IPR002181; Fibrinogen_C.
  DR Pfam: PF00147; fibrinogen_C.
  DR SMART; SM00186; Fbg; 1.
  DR PROSITE; PS00514; FIBRIN_AG_C-DOMAIN; 1.
  SQ SEQUENCE 495 AA; 56848 MW; EBFAC3ABF1P08F6 CRC64;

Query Match          19.1%; Score 382; DB 4; Length 495;
Best Local Similarity 26.4%; Pred. No. 2.7e-23;
Matches 110; Conservative 73; Mismatches 138; Indels 96; Gaps 16;

OY 3 VQGNQVHHSTDDSVYNIVEDGSNADESKSNDYVCKEDCESSCDVTKI-----TREE--- 55
Db 112 IQQNAVQNT-----AVMEIGINLNLQI-----AEQTRKLTDEAOVLAQOTRIELQL 160
OY 56 -KHFCRN-LQNSIVSYSTRSKL-----LRNMDQQAASL 89
Db 161 LEHSLSTNKKLEQILDDQISEINKLQDKNSPLEKKVLAMEDKHIIQLQSKREKQQLQVLY 220
OY 90 DYLSNQVMEILNKRVLNLT--TEVPRKQ-----LDPRPHRVSQHG 127
Db 221 SKQNSIIIELEKELIYATAVNVNSVLQKQOHDIMETVNNLLTMASTNSKSDPRVAKEEQISF 280
OY 128 LDCTGIIKIDTIGSVTRTPSGSLVLIHPEGSSYPEVWCMDYDGGGWTYQKRIDGIDFOR 187
Db 281 RDCAEVFS-----GTTNGIYITLTTPNSTEELKAYCDMEAGGGWTIIQKREDSVDFOR 336
OY 188 LWCIDYLDGFDLLGEBFWGLKRIEYIVNQKTSFMYLVYALESEDDTLVASYADNFWLEDE 247
Db 337 TWKEKVGFGNSGSGYWGNEFVSQLTNGQR--YVLKTHLDMGSENAVSLYEHFYLSSE 394
OY 248 TRFEFMHIGRISGNAAGDAFRGLKAKCDNQNAMPFSTSDVNDGCRPACLVQSAVSCSHL 307
Db 395 ELNYIHHILKGLTGTGKI-----SSISQPGNDFSTKDDNDKDC-----LCKCSQM 439
OY 308 HNKTMWMEGGLANLNGIHH-----FSGKLATLGIOMGTWTKNNSPVKYSVKIR 360
Db 440 LT-GGWMPDADGCPNSLNGMYTPQKQNTNKF--NGIKWYV--KSGSISLAKYTTMIR 491

RESULT 8
O43827
ID O43827 PRELIMINARY; PRT; 346 AA.
AC O43827;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE CDP6 (Angiopoietin-1like factor) (CDP6 protein).
GN D3647M6.1 OR CDP6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN
  RP SEQUENCE FROM N.A.
  RM TISSUE=CORNEA;
  RA Peek R., van Gelderen B.E., Bruinenberg M., Kijlstra A.;
  RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

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DB 452 TWDMAKHGTDDGYVMNMW--KDSWYSMKKMSIKIR----PYF 487

RESULT 12
Q9DER2

ID Q9DER2 PRELIMINARY; PRT: 493 AA.

AC Q9DER2; 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Angiopoietin-2A.
GN ANGIOPOIETIN-2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20422311; PubMed=10964717;
RA Mezquita J., Mezquita P., Montserrat P., Mezquita B., Franccone V.,
Vilagrasa X., Mezquita C.;
RT "Genomic structure and alternative splicing of chicken angiopoietin-2";
RL Biochem. Biophys. Res. Commun. 275:643-651(2000).
DR EMBL; AJ289777; CAC08174.1; -.
DR HSSP; P02671; 1FZD.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 493 AA; 56393 MW; BDIA21F90172F6DA CRC64;

Query Match 18.9%; Score 378.5; DB 13; Length 493;
Best Local Similarity 26.4%; Pred. No. 5.2e-23;
Matches 112; Conservative 68; Mismatches 135; Indels 109; Gaps 17;

QY 3 VQGNCHVHSTDSVNVNVEDGSKAKDESKNDTVCKEDCESCDVKKITREEKHFMCRN 62
DB 109 IQOTAVQNGT-----AVMIEIGTNLNTQ-----ABQTRKLTVDVQAVLNQTRLEQL 157
QY 63 LQNSIVSYSTYKTLR-----NMDEQASLDYLSQVNEL----- 99
DB 158 LEHSL-----STNKLEROISVQTNETIKLOEKNSFLKRVLEMEDKHTLQKSIKERDQ 212
QY 100 -----MNVL-----LITTEVFRKQLDPPHRYQS--HGL----- 128
DB 213 LQYLVARQNSIIIELEKQVLTATVNSVLOKQCHDLMETVHNLMTSTPSAKNFIAK 272
QY 129 -----DCTD-IKDTIGSVTKTPSGLYIHPGESSYPFEVMDMDYRGGWTVIQRID 180
DB 273 EEOISFQKCAEAFKSGL-----TSGIYTLTFPNSAQEKAYCDMESNGGWTVIQRRED 327
QY 181 GIIDFOLKCDYLDGFEYDLGEFYLGLKIFYYINOKNTSPMLYVALESEDDTLATASYD 240
DB 328 GSYDFHTFWKEYKGFDPAGEYWLGNFWSQLTKR--YVLTIIILKDWEGNAYTLYD 385
QY 241 NFWLEDETREFKMHGIRYSGNAGDAFRGLKEDNONAMPSTSDVDNDCGRPACTLVNGQS 300
DB 386 QFYLANEOKYRIHLKGLTGTAKI-----SSISQPGNDSTKADNDKC----- 430
QY 301 VKSCSHLHNTGWNFNEGLANGIIH---FSGKLATGCIOWGTWKNNSPYKIKSVS 356
DB 431 ICKSQMLT--GGWFPDAGCPNSLNGMYTPLRQNNKF--NGIKWYV--KSGYSLKATY 485
QY 357 MKIR 360
DB 486 MKIR 489

RESULT 13
Q9DER0 PRELIMINARY; PRT: 441 AA.

AC Q9DER0;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Angiopoietin-2C.
GN ANGIOPOIETIN-2C.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20422311; PubMed=10964717;
RA Mezquita J., Mezquita P., Montserrat P., Mezquita B., Franccone V.,
Vilagrasa X., Mezquita C.;
RT "Genomic structure and alternative splicing of chicken angiopoietin-2";
RL Biochem. Biophys. Res. Commun. 275:643-651(2000).
DR EMBL; AJ289779; CAC08176.1; -.
DR HSSP; P02671; 1FZD.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 441 AA; 50472 MW; DC98127FEOCE34E2 CRC64;

Query Match 18.8%; Score 376.5; DB 13; Length 441;
Best Local Similarity 30.3%; Pred. No. 6.6e-23;
Matches 101; Conservative 61; Mismatches 122; Indels 49; Gaps 14;

QY 40 DCEESCVCVKITREEKH---FMCRLQNSIVSYTRS---TKLIRNMDEQASLDYL 92
DB 142 EMEKHKLQKLSIKEDNQQLVAVR--QNSIIIELEKQVLTATVNSVLOKQCHD--- 196
QY 93 SNOYELMNRVLLITTEVFRKQLDPPHRYQSHGLDCTD-IKDTIGSVTKTPSGLYI 151
DB 197 ---METVHNLMTSTPNSAK--NFAKEOISFKCAEAFKSGL-----TSGIYTLT 246
QY 152 PEGSSYFEVWCDMDYGGGWTVIQRIDGIIDFQRLMCOYLDGFGDLGFWGLKIF 211
DB 247 FPNASQEKAYCDMESNGGWTVIQRREDGSDVDHRTWKEKIFGDPAGEYWLGNFVS 306
QY 212 YIVNOKNTSPMLYVALESEDDTLAVASYDNFWEDETRFFKMHGIRYSGNAGDAFRGLK 271
DB 307 QLTNQKR--YVLTIIILKDWEGNEAYTLYDQFYLANEOKYRIHLKGLTGTAKI-----S 359
QY 272 EDNONAMPSTSDVDNDCGRPACTLVNGQSVKCSHLLHNTGWNFNEGLANGIIH--- 328
DB 360 SISQPGNDFSTKADNDKC-----ICKSQMLT--GGWFPDAGCPNSLNGMYTPLR 408
QY 329 -FSGKLATGCIOWGTWKNNSPYKIKSVKIR 360
DB 409 QNNKF--NGIKWYV--KSGYSLKATYMKIR 437

RESULT 14
Q9D8W6 PRELIMINARY; PRT: 308 AA.
AC Q9D8W6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Tachylectin-5B isoform.
OS Tachylectin tridentatus (Japanese horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachypleus.
OX NCBI_TaxID=6853;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398666; PubMed=10468566;
RA Gokudan S., Muta T., Tsuda R., Koori K., Kawahara T., Seki N., Mizuno Y., Wai S.N., Iwanaga S., Kawabata S.;

QY 110 -----VFRKO---LDP-----FPHRPVOSHGL----- 128
DB 188 NOSVMTLLEBCLRFHSQDTHVSPPLVQVYPQHIPNSQOYTPGLGNETIQRDGPYR 247
QY 129 DCTDIKIDTIGSVTKTP-----SGLYIIHPGSSYFPEV 161
DB 248 DLMPPDLATSTPSTKSPFKIPVTFINEGPFKDCQOAKKEAGHSVSGIYMKPENSNGPML 307
QY 162 MCDMDYRGCGMTVIOKRDIGDIIDFQRLMCDYLDGFGDLGEEWLGKTFYVNOKNTSF 221
DB 308 KCENSIDPEGMTVIOKRDIGSVNFFRNMENYKKGFGNIDGFWLGJENIYMLSDNODN--Y 365
QY 222 MLYVALESEDDTLAASVDNFWLEDETRFKNHILGRYSGNADAFRGKLKEDNONAMPFS 281
DB 366 KLLIELEDMDSKRYAEYSFRLPESEFYRLRLGTGQNADDSMMW-----HNGKQFT 419
QY 282 TSDVDNDGCRPACLVNGOSVSKSHLNKTMGFNECGLANLNGIHHSKTLA--TGI 338
DB 420 TLDROKD-----MYAGNCAHFH-KGWMYNACAHSNLNGWYRGHYRSRKHODGI 468
QY 339 OMGTWTKNNSPVKIKSVSKIR 360
DB 469 FWAEX--RGGSYSLRAVOMMIK 488

RESULT 2

US-08-960-507-4
; Sequence 4, Application US/08960507
; Patent No. 6057435
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960.507
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-960-507-4

Query Match 21.2%; Score 425; DB 3; Length 491;
Best Local Similarity 26.9%; Pred. No. 3.2e-37;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

QY 24 SNAKESKSNIDVCKEDECSDVTKTITRE-EKHFMCRNLONSIVSTRSTKILLRMM 82
DB 68 TKGDASTIKDMITMDLENLKDVLRSOKREIDVQLVVDGNIVNEVKKLLRKESRNMN 127

QY 83 DE-QQASIDYL-----SNQVNEIMNRVLLTTE----- 109
DB 128 SRVTOLYMOLHEIIRKRDNSLELSOLENKLIVTTEMLKMATRYRELEVKYASLTDLVN 187
QY 110 -----VFRKO---LDP-----FPHRPVOSHGL----- 128
DB 188 NOSVMTLLEBCLRFHSQDTHVSPPLVQVYPQHIPNSQOYTPGLGNETIQRDGPYR 247
QY 129 DCTDIKIDTIGSVTKTP-----SGLYIIHPGSSYFPEV 161
DB 248 DLMPPDLATSTPSTKSPFKIPVTFINEGPFKDCQOAKKEAGHSVSGIYMKPENSNGPML 307
QY 162 MCDMDYRGCGMTVIOKRDIGDIIDFQRLMCDYLDGFGDLGEEWLGKTFYVNOKNTSF 221
DB 308 KCENSIDPEGMTVIOKRDIGSVNFFRNMENYKKGFGNIDGFWLGJENIYMLSDNODN--Y 365
QY 222 MLYVALESEDDTLAASVDNFWLEDETRFKNHILGRYSGNADAFRGKLKEDNONAMPFS 281
DB 366 KLLIELEDMDSKRYAEYSFRLPESEFYRLRLGTGQNADDSMMW-----HNGKQFT 419
QY 282 TSDVDNDGCRPACLVNGOSVSKSHLNKTMGFNECGLANLNGIHHSKTLA--TGI 338
DB 420 TLDROKD-----MYAGNCAHFH-KGWMYNACAHSNLNGWYRGHYRSRKHODGI 468
QY 339 OMGTWTKNNSPVKIKSVSKIR 360
DB 469 FWAEX--RGGSYSLRAVOMMIK 488

RESULT 3

US-09-136-828-4
; Sequence 4, Application US/09136828
; Patent No. 6350450
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136.828
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130R1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-136-828-4

Query Match 21.2%; Score 425; DB 4; Length 491;
Best Local Similarity 26.9%; Pred. No. 3.2e-37;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

QY 24 SNAKESKSNIDVCKEDECSDVTKTITRE-EKHFMCRNLONSIVSTRSTKILLRMM 82

Db 68 TKGDASTIKDMITRMDLENLKDVLRSKQREIDVLDLVVDGNIVNEVLLRKESNNM 127
QY 83 DE-QQASLDYL-----SNQVNEIMNRVLLTTE----- 109
Db 128 SRVQLYMQLLHETIRKRDNSLELSOLENKILNVTTEMLKMATRYRELEVYASLDLVN 187
QY 110 -----VFRKO---LDP-----FPHRPVOSHGL----- 128
Db 188 NQSVMITLLEECRLRISRODTHVSPPLVQVPOHIPSQOQYTPGLLGNEIQRPDGPYR 247
QY 129 DCTDIDKDTIGSVTKTP-----SGLYIHPGSSYPRFV 161
Db 248 DLMPPPLATSPKSPKIPPVTFINEGPPKDCQQAKEAGHSVGIYMIKRPENSGPMOL 307
QY 162 MCDMDYRGSGMTYQKRIIDIFQRLMCDYLDGFDLLGEFVGLKKIFYIYNQKTSF 221
Db 308 WCENSIDPGGWYIQRKTDSSVNFERNMENTKKGFGNIDETWGLGENTIMLSQDN--Y 365
QY 222 MLYVALESEDDTLAYASYDNFMLEDETFRFPMHLGRYSNAGDAFRGLKEDNONAMPFS 281
Db 366 KLIIELEDMQDKRYAYESSFRLEPESEFYRLRGTGYQNAQDSMM-----HNGKQFT 419
QY 282 TSDVDNDGCRPACLVNGQSVKSCSHLNKTGMFNEBGLANLNGIHFSKLLA---TGT 338
Db 420 TLDRDKD-----MYAGNCAHFH-KGGMWYNACAHSLNGLVWYRGHYRSKHODGI 468
QY 339 QMGWTKNNSPVKIKSVSMKIR 360
Db 469 FMAEY--RGSYSILRAVQMMIK 488

RESULT 4
US-09-332-928A-4
Sequence 4, Application US/09332928A
Patent No. 6368853

GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
Gurney, Austin L.

TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/332.928A

FILING DATE: 14-Jun-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/933,821

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Ginger R.

REGISTRATION NUMBER: 33,055

REFERENCE/DOCKET NUMBER: P1130

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/952-9881

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 491 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-332-928A-4
Query Match 21.2%; Score 425; DB 4; Length 491;
Best Local Similarity 26.9%; Pred. No. 3.2e-37;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

QY 24 SNAKDESKNDYCKEDCEESCDYKTKITRE-EKHFRCRLQNSIYSTSTKLLRNM 82
Db 68 TKGDASTIKDMITRMDLENLKDVLRSKQREIDVLDLVVDGNIVNEVLLRKESNNM 127
QY 83 DE-QQASLDYL-----SNQVNEIMNRVLLTTE----- 109
Db 128 SRVQLYMQLLHETIRKRDNSLELSOLENKILNVTTEMLKMATRYRELEVYASLDLVN 187
QY 110 -----VFRKO---LDP-----FPHRPVOSHGL----- 128
Db 188 NQSVMITLLEECRLRISRODTHVSPPLVQVPOHIPSQOQYTPGLLGNEIQRPDGPYR 247
QY 129 DCTDIDKDTIGSVTKTP-----SGLYIHPGSSYPRFV 161
Db 248 DLMPPPLATSPKSPKIPPVTFINEGPPKDCQQAKEAGHSVGIYMIKRPENSGPMOL 307
QY 162 MCDMDYRGSGMTYQKRIIDIFQRLMCDYLDGFDLLGEFVGLKKIFYIYNQKTSF 221
Db 308 WCENSIDPGGWYIQRKTDSSVNFERNMENTKKGFGNIDETWGLGENTIMLSQDN--Y 365
QY 222 MLYVALESEDDTLAYASYDNFMLEDETFRFPMHLGRYSNAGDAFRGLKEDNONAMPFS 281
Db 366 KLIIELEDMQDKRYAYESSFRLEPESEFYRLRGTGYQNAQDSMM-----HNGKQFT 419
QY 282 TSDVDNDGCRPACLVNGQSVKSCSHLNKTGMFNEBGLANLNGIHFSKLLA---TGT 338
Db 420 TLDRDKD-----MYAGNCAHFH-KGGMWYNACAHSLNGLVWYRGHYRSKHODGI 468
QY 339 QMGWTKNNSPVKIKSVSMKIR 360
Db 469 FMAEY--RGSYSILRAVQMMIK 488

RESULT 5
US-09-136-801-4
Sequence 4, Application US/09136801
Patent No. 6413770.

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth

APPLICANT: Botstein, David

APPLICANT: Goddard, Audrey

APPLICANT: Roy, Margaret

APPLICANT: Ferrara, Napoleone

APPLICANT: Tumas, Daniel

APPLICANT: Schwall, Ralph

TITLE OF INVENTION: Tie Ligand Homologues

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/136,801

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Ginger R.

```

; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130B2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-136-801-4

```

```

Query Match          21.2% Score 425; DB 4; Length 491;
Best Local Similarity 26.9% Pred. No. 3,2e-37;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

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QY 24 SNAKDESKNDTVCKEDCEESCDVKTITRE-EKHEMCHNLONSIVSYSTRSKLLRNMM 82
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 68 TKGODASTIKDMITRMDLENLKDVLRSQKREIDVQLVVDVGNTVNEVKLLRKESRNN 127
QY 83 DE-QQASLDYL-----SNQVNLNMRVLLTTE----- 109
DB 128 SRVTLQYMLLHEILIRKRDNSLELSQLENKILNVTEMLKMATRYELEVKYASLTDLVN 187
QY 110 -----VFRKO---LDP-----FPHRPVOSHGL----- 128
DB 188 NOSVMTLLEEOCLRTFSKQDTHVSPPLVQVVPQHPIPSQOYTPGLLGNETORDPGYR 247
QY 129 DCTDIKDTIGSVYTKRP-----SGLYIHPGSSYPEV 161
DB 248 DLMPRPDLATSPTKSPFKIPVYTFINEGPFKDCQQAKEAGHSVSGLYMKRPENSGPMQL 307
QY 162 MCDMDYRGCGWTVIOKRIDGITDFQRLWCDYLDGFODLIGEEWLGKIKFTYVNOKNTEF 221
DB 308 WENSILDPGCVTVIOKRIDGSVNFPRMWNENYKKGCGNIDGEYWLGLNENTYMLSDN--Y 365
QY 222 MLYVALESDDTLAASVDFWLEDETRFEKMHILGRYSNAGDAFGLKKEKNONAMPSS 281
DB 366 KLLIELEMSDKKVAEYSSFRLEPSEFYRLGLTYGQNAQDSMMW-----HNGKOPT 419
QY 282 TSDVDNDGCRPACLVNGOSVKSCHLNKTMWPFNECGLANLNGIHFSGKLLA--TGI 338
DB 420 TLDROKD-----MYAGNCAHFH-KGWMYNACAHSNLNGVYRGHYSRKHODGI 468
QY 339 QMGWTWKNNSPVKIKSVSMKIR 360
DB 469 FWAEEY--RGGSYSLRVQMMIK 488

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RESULT 6
US-09-332-929-4
; Sequence 4, Application US/09332929
; Patent No. 6420542
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/332,929
; FILING DATE:

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/933,821
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Glaser R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-332-929-4

```

```

Query Match          21.2% Score 425; DB 4; Length 491;
Best Local Similarity 26.9% Pred. No. 3,2e-37;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

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QY 24 SNAKDESKNDTVCKEDCEESCDVKTITRE-EKHEMCHNLONSIVSYSTRSKLLRNMM 82
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 68 TKGODASTIKDMITRMDLENLKDVLRSQKREIDVQLVVDVGNTVNEVKLLRKESRNN 127
QY 83 DE-QQASLDYL-----SNQVNLNMRVLLTTE----- 109
DB 128 SRVTLQYMLLHEILIRKRDNSLELSQLENKILNVTEMLKMATRYELEVKYASLTDLVN 187
QY 110 -----VFRKO---LDP-----FPHRPVOSHGL----- 128
DB 188 NOSVMTLLEEOCLRTFSKQDTHVSPPLVQVVPQHPIPSQOYTPGLLGNETORDPGYR 247
QY 129 DCTDIKDTIGSVYTKRP-----SGLYIHPGSSYPEV 161
DB 248 DLMPRPDLATSPTKSPFKIPVYTFINEGPFKDCQQAKEAGHSVSGLYMKRPENSGPMQL 307
QY 162 MCDMDYRGCGWTVIOKRIDGITDFQRLWCDYLDGFODLIGEEWLGKIKFTYVNOKNTEF 221
DB 308 WENSILDPGCVTVIOKRIDGSVNFPRMWNENYKKGCGNIDGEYWLGLNENTYMLSDN--Y 365
QY 222 MLYVALESDDTLAASVDFWLEDETRFEKMHILGRYSNAGDAFGLKKEKNONAMPSS 281
DB 366 KLLIELEMSDKKVAEYSSFRLEPSEFYRLGLTYGQNAQDSMMW-----HNGKOPT 419
QY 282 TSDVDNDGCRPACLVNGOSVKSCHLNKTMWPFNECGLANLNGIHFSGKLLA--TGI 338
DB 420 TLDROKD-----MYAGNCAHFH-KGWMYNACAHSNLNGVYRGHYSRKHODGI 468
QY 339 QMGWTWKNNSPVKIKSVSMKIR 360
DB 469 FWAEEY--RGGSYSLRVQMMIK 488

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RESULT 7
US-09-442-143A-2
; Sequence 2, Application US/09442143A
; Patent No. 6403089
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; APPLICANT: Clark, David A.
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-14
; CURRENT APPLICATION NUMBER: US/09/442,143A
; CURRENT FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 60/046,537
; PRIOR FILING DATE: 1997-05-17
; PRIOR APPLICATION NUMBER: US 60/061,684
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2

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; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens fg12
US-09-442-143A-2

Query Match
Best Local Similarity 30.2%; Score 413.5; DB 4; Length 439;
Matches 119; Conservative 61; Mismatches 147; Indels 67; Gaps 15;

QY 14 SSVNIVEDSGNAKDESKNDYCKEDCE-----ESCQVYTK 50
D 73 SRIEVEKEVONLKEIYNSLKSC-QDCKQADNDGDPGRNGLLPSTGAPGEVDNRVR 131
QY 51 ITREBEKHEKCRNIQNS-----IVSYTRSTKTLRNM-----MDEQAQSLDYLSNQVNELM 100
D 132 ELSEEVNKLSESELKNAKEEINVLHGRLEKILVNMNIENYVDSKRVANLFEVYNSLGKC 191
QY 101 NRYVLLITTEFRKQJDFPHRPVOSHGL--DCDIDKDTIGSYVTKTPSGLYTIHPESSSY 158
D 192 SKC-----PSQEQIQSRPVO-HLITYKDCSDY---AIGRSSEYTRVTPDPKNS 237
QY 159 FEVWCDMDYRGGWTVYQKRIIDGIIDPQRLMCDYLDGFGLAGEFWLKKIFYIVNQKN 218
D 238 FEVYCDMEHMGGWTVQANLDSNTFRTRMODYKAGFNLRRREFWGNCKIHLLT--KS 295
QY 219 TSFMYALASEDDTLAYASTYDNFLEDETFEFKMLGRYSGNAGDAFRGLKEDNQNM 278
D 296 KEMILRIDLEDVNGVELYALYDQFYVANEFLKYLRLHVGNYNGTAGDALR-FNKHYNHDLK 354
QY 279 PFESVDNDGCRACALYVNOQSVKSCSHLNKYGWMEGCLANLNG-IHFSKLLATG 337
D 355 FETTPDKNDNRYPBG-----NCG-LYSSGWMFDCALSLANLNGKYHOKYRGVANG 404
QY 338 IOMGTW--TKNSPVKIKSYSMKIRRYNP-YFK 368
D 405 IFMGTWGVSEAHFPGYKSSFKKAKMIRKHKR 438

RESULT 8
US-09-442-143A-4
; Sequence 4, Application US/09442143A
; Patent No. 6403089
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-14
; CURRENT APPLICATION NUMBER: US/09/442,143A
; CURRENT FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 60/046,537
; PRIOR FILING DATE: 1997-05-17
; PRIOR APPLICATION NUMBER: US 60/061,684
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Murine fg12
US-09-442-143A-4

Query Match
Best Local Similarity 20.3%; Score 405.5; DB 4; Length 432;
Matches 110; Conservative 43; Mismatches 115; Indels 43; Gaps 13;

QY 78 LRNMNDEQA-----SIDYLSNOVNELMNRYVLLITTEFRKQD-----PFP 119
D 137 LRNKKDDIQIGRLGLETLHLVNMNIENYVDMRYANLTVVY--NSLDGKCSKCSQSEHMQ 194
QY 120 HRPVOSHGL--DCDIDKDTIGSYVTKTPSGLYTIHPESSSYFEVWCDMDYRGGWTVYQK 177
D 195 SQPVQ-HLITYKDCSD-HYVIG---RSSGAYRYTPDHRNSSFEVYCDMEHMGGWTVYQ 249
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QY 178 RIDGIIDFORIMCDYLDGFGLAGEFWLGLKIFYIVNQKNTSMALYALESEDDTLAYA 237
D 250 RLDSSTNFTREMKDYKAGFNLREFFWLGNDKIHLLT--KSKEMILRIDLEDVNGLTLVA 307
QY 238 SYDNFWELEDETFEFKMLGRYSGNAGDAFRGLKEDNQNMPESTSDVNDGCRPALVN 297
D 308 LYDQFYVANEFLKRLHIGNGTAGDALR-FSHYVNHDLRFTTPRDNDRYPBG---- 362
QY 298 GQSVKSCSHLNKYGWMEGCLANLNG-IHFSKLLATGIGWTVTKNN--SPVKIKS 354
D 363 -----NCG-LYSSGWMFDCALSLANLNGKYHOKYRGVANCIFMGTWPGINQAPGCKS 416
QY 355 VSMKIRRYNP 365
D 417 SFKQAKMIRP 427

RESULT 9
US-08-740-223A-12
; Sequence 12, Application US/08740223A
; Patent No. 6265564
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: Expressed ligand - Vascular
; TITLE OF INVENTION: Intercellular Signalling Molecule
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/740,223A
; FILING DATE: 25-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US9N 60/022/999
; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Coberc, Robert J
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 333
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-345-7400
; TELEFAX: 914-345-7721
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 490 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: hTTL
; LOCATION: 1...490
; OTHER INFORMATION: human TIE-2 ligand 1
US-08-740-223A-12

Query Match
Best Local Similarity 20.3%; Score 405.5; DB 4; Length 490;
Matches 118; Conservative 65; Mismatches 125; Indels 121; Gaps 16;

QY 3 VQCGVHAHSDSSVNVNIVEGSGNAKDESKNDYCKEDCESQVYTKTRREKHEKCRN 62
D 108 IQNNAVONHT---ATMLEGTSLISOT-----AQTRKLDIVETOVNLQTSRLQTL 156
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OY 63 LONSIYSV-----TRSTFKLLRNMM 82
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DB 157 LENSLSSTYKLEKQLLOQTNEILKIHKNSLLEKILLEMCKHKEELDTLKEEKENLQGLV 216
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DB 217 TROTYYIIOLEKQLNATNNNSVLOKQOLEMDTVNHLNVLCTKEVLLGKGRKEEKP- 275
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DB 276 -----RDCADVY-----QAGFNKSGITYITIYINNPEPKKVCNMDVNGGTVIQHRE 323
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DB 324 DGSLDPRQKWKKEYKMGFGNPSGEYWLGNFEIFAITSQR--QVWLRIELMDWEGNRAVSQY 381
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OY 240 DNFWEDETRFRFKMLGRYSNGNAGDAFRGLKKEDN--QNAPESTSDVNDGCRPAC--L 295
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DB 382 DRFHIGNEKQNRRLYLKGTGTAG-----KQSSLILHGADEFSTKDADNDNCMKCALM 434
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US-09-709-188-12
; Sequence 12, Application US/09709188
; Patent No. 6441137
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular InterCellular Signaling Molecule
; FILE REFERENCE: REG 333-Z
; CURRENT APPLICATION NUMBER: US/09/709,188
; PRIORITY FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIORITY FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-709-188-12
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Query Match 20.3%; Score 405.5; DB 4; Length 490;
Best Local Similarity 27.5%; Pred. No. 4,1e-35;
Matches 118; Conservative 65; Mismatches 125; Indels 121; Gaps 16;

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DB 108 IOONAVQNHNT-----ATMLEIGTSLSQT-----AEQTRKLTVDVETOVLANQTSRLQIDL 156
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DB 157 LENSLSSTYKLEKQLLOQTNEILKIHKNSLLEKILLEMCKHKEELDTLKEEKENLQGLV 216
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OY 83 DEQOASLDLYSNQVN-----ELM-----NRVLLLTTEVF-----RKOLDPPP 119
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DB 217 TROTYYIIOLEKQLNATNNNSVLOKQOLEMDTVNHLNVLCTKEVLLGKGRKEEKP- 275
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OY 120 HRPVOSHGLDCTDIKDTISVTKTPSGLYTIHPEGSSYFEVWCDMDYGGCTVYQKRI 179
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DB 324 DGSLDPRQKWKKEYKMGFGNPSGEYWLGNFEIFAITSQR--QVWLRIELMDWEGNRAVSQY 381
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OY 240 DNFWEDETRFRFKMLGRYSNGNAGDAFRGLKKEDN--QNAPESTSDVNDGCRPAC--L 295
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OY 296 VNGQSVKSCSHLHNTKGMWFNECGLANLNGIHHS-----GKLLATIGQWGTWKNNSPVK 351
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DB 435 LFG-----GWMFADAGPSNLGMFTYAGQNHGKL--NGIKWHYF--KGPSYS 477
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OY 352 IKSVMKIR 360
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DB 478 IRSTTMIR 486
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RESULT 11
US-08-740-223A-4
; Sequence 4, Application US/08740223A
; Patent No. 6265564
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/740,223A
; FILING DATE: 25-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/022/999
; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Coibert, Robert J
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 333
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-345-7400
; TELEFAX: 914-345-7721
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 497 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; FEATURE:
; NAME/KEY: Human TIE-2 ligand 1
; LOCATION: 1...2146
; OTHER INFORMATION: from T986 clone
US-08-740-223A-4
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Query Match 20.2%; Score 403.5; DB 4; Length 497;
Best Local Similarity 27.3%; Pred. No. 6,9e-35;
Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

OY 3 VOCNCVHSTDSVNIIVEDGSNAKDESKSNDTVCKEDCESCDVYKTRTREKHPMCRN 62
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DB 115 IOONAVQNHNT-----ATMLEIGTSLSQT-----AEQTRKLTVDVETOVLANQTSRLQIDL 163
|:|:|:|:|
OY 63 LONSIYSV-----TRSTFKLLRNMM 82
|:|:|:|:|
DB 164 LENSLSSTYKLEKQLLOQTNEILKIHKNSLLEKILLEMCKHKEELDTLKEEKENLQGLV 223
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Db 308 WCENSLDPGGMTVIOKRIDGVSNEFRMMENYKRGFGNIGDEYVLGENTYMLSDQDN--Y 365
Qy 222 MLYVALESDDTDLAASYDNFWELEDTREFKMLHGRYSNAGDAFRGLKEDNQNMPS 281
Db 366 KLILEEDMSDKKYAEVSSFRLEPESEYRLRLGTYYQGNADSDMMW-----HNGKQFT 419
Qy 282 TSDVDNDGCRPACLVNGOSVSKSHLHNTGWMFNECGLANINGIHFSGLKLA--TGI 338
Db 420 TLDROKD-----WYAGNCAHFN-KGWMYNACANSLNNGVYRGHTRSKHODCI 468
Qy 339 OMTGTTKNSPVKIKSVSKIR 360
Db 469 FWAEX--RGGSYSLRAVOMMIK 488

RESULT 2
US-10-179-744-4
; Sequence 4, Application US/10179744
; Patent No. US20020173627A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Samuel et al.
; TITLE OF INVENTION: TIE-2 LIGANDS, METHODS OF MAKING AND USES THEREOF
; FILE REFERENCE: REG 330-F-PCT-US
; CURRENT APPLICATION NUMBER: US/10/179,744
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US/08/817,318
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
US-10-179-744-4

Query Match 20.1%; Score 402.5; DB 9; Length 497;
Best Local Similarity 27.3%; Pred. No. 2,4e-30;
Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

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Qy 63 LQNSIVSY-----TRSTRKLLRNMM 82
Db 164 LENSISTYKLEKQLIQOTNEILIKHEKNSLHEKILTEMEGKHKEELDTLKEKENIQGLV 223
Qy 83 DEQOASLDYLSNQVN-----ELM-----NRVLLTTEYF-----RKOLDPPR 119
Db 224 TRQYTIIELEKQLNRATYNNVSLQKQOLEMDYVHNLYNLCTKVELLKGKREKEKRP- 282
Qy 120 HRPVOSHGLDCTDIDKTIGSVTKTPSGLYIHPESSSYPFEVCMCDMDYRGSGMTYIQKRI 179
Db 283 -----RDCADYV-----QAGFNKSGIYTYIINNPEPKKFCVCMNDVGGGWTYIQHRE 330
Qy 180 DGIIDFORLWCDYLDGEGDILGEFVLGKTKFYVNOQNTSFMLYVALESDDTLATASY 239
Db 331 DGSLDFOGKWEYKMGFGNPGSEYWLGNFEIFAITSQR--QYMLRELMDWEGNRAYSQY 388
Qy 240 DNFWLEDETRFFKMLHGRYSNAGDAFRGLKEDN--ONAMFSTSDVNDGCRPAC--L 295
Db 389 DRFHIGNEKQNRRLYLKHTGTAG-----KQSSILLHGADFSTRKADNDNDCMCKCALM 441
Qy 296 VNGOSVSKSHLHNTGWMFNECGLANINGIHFS--GKLLATGIOWGTGTTKNSPVK 351
Db 442 LTG-----GWMFIDACGPSNLNGMFTYAGQNNHKL--NGIKNHYF--KGPSYS 484

Qy 352 IKSVMKIR 360
Db 485 LRSTYMIIR 493
RESULT 3
US-10-066-500-4
; Sequence 4, Application US/10066500
; Patent No. US20020177165A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gottfriesen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3130RIC7
; CURRENT APPLICATION NUMBER: US/10/066,500
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059588
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; PRIOR APPLICATION NUMBER: 60/074086
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074092
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/081049

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14	PRIOR APPLICATION NUMBER: 60/106032
15	PRIOR FILING DATE: 1998-10-28
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20	PRIOR APPLICATION NUMBER: 60/139695
21	PRIOR FILING DATE: 1999-06-15
22	PRIOR APPLICATION NUMBER: 60/145070
23	PRIOR FILING DATE: 1999-07-20
24	PRIOR APPLICATION NUMBER: 60/145698
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26	PRIOR APPLICATION NUMBER: 60/149366
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28	PRIOR APPLICATION NUMBER: 60/169495
29	PRIOR FILING DATE: 1999-12-07
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33	PRIOR FILING DATE: 1997-09-19
34	PRIOR APPLICATION NUMBER: 08/960507
35	PRIOR FILING DATE: 1997-10-29
36	PRIOR APPLICATION NUMBER: 09/114844
37	PRIOR FILING DATE: 1998-07-14
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42	PRIOR APPLICATION NUMBER: 09/136838
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62	PRIOR APPLICATION NUMBER: 09/330755
63	PRIOR FILING DATE: 1999-06-14
64	PRIOR APPLICATION NUMBER: 09/380137
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67	PRIOR FILING DATE: 1999-08-25

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PRIOR FILING DATE:	2000-03-09
PRIOR APPLICATION NUMBER:	09/548815
PRIOR FILING DATE:	2000-04-13
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PRIOR FILING DATE:	2000-09-18
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PRIOR FILING DATE:	2001-03-09
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PRIOR APPLICATION NUMBER:	09/866028
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PRIOR FILING DATE:	2001-05-30
PRIOR APPLICATION NUMBER:	09/872035
PRIOR FILING DATE:	2001-06-01
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PRIOR FILING DATE:	2001-06-19
PRIOR APPLICATION NUMBER:	09/US98/14552
PRIOR FILING DATE:	1998-07-14
PRIOR APPLICATION NUMBER:	PCT/US98/188824
PRIOR FILING DATE:	1998-09-10
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PRIOR FILING DATE:	1998-11-25
PRIOR APPLICATION NUMBER:	PCT/US99/050288
PRIOR FILING DATE:	1999-03-08
PRIOR APPLICATION NUMBER:	PCT/US99/12252
PRIOR FILING DATE:	1999-06-02
PRIOR APPLICATION NUMBER:	PCT/US99/20111
PRIOR FILING DATE:	1999-09-01
PRIOR APPLICATION NUMBER:	PCT/US99/205944
PRIOR FILING DATE:	1999-09-08
PRIOR APPLICATION NUMBER:	PCT/US99/21090
PRIOR FILING DATE:	1999-09-15
PRIOR APPLICATION NUMBER:	PCT/US99/21547

Query Match	20.0%;	Score 400;	DB 9;	Length 493;
Best Local Similarity	31.9%;	Pred. No. 4.1e-30;		
Matches 94;	Conservative 50;	Mismatches 93;	Indels 58;	Gaps 11

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Db   279 L Q A E D G H D I S S I L A K E N T N R I M Q W C D R H D P G W T Y Q R L D S V N F R M W E T Y K Q 338
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QY 63 LONSIYSV-----TRSTKLLRNM 82
   164 LENSLSYKLEKOLLQOTNEILKHEKNSLLEHKLLEMEGKHKELDPTLKEKENLOGLV 223
QY 83 DEQOASLDYLSNOVN-----ELM-----NRVLLLTVEF-----RKOLDPF 118
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QY 119 PHRVOSHGLDCTDIKDTIGSVTKTPSGLYIIPREGSSYPFEVWCDMDYRGCGWTYIOKR 178
   284 -----RDCADYV-----QAGFNKSGITYITYINNMPREKKYFCANDVGGCGWTYIOHR 330
QY 179 IDGIIDFORIMCDYLDGFGDLGFEWLGKFIYIVNOKNTSFMLYVALESEDPTLAYAS 238
   DB 284 -----RDCADYV-----QAGFNKSGITYITYINNMPREKKYFCANDVGGCGWTYIOHR 330
QY 331 EDGSLDFORGMKEKYMFGNPSGEYWLGNFEIFAITSOR--QYMLRIELMDWEGNRAYSQ 388
QY 239 YDNFWLEDETRFEFKMLHGRISGNAGDAFRGLKEDN--QNAAMPSTSDVNDGCRPAC-- 294
   DB 389 YDRFHIGNEKQNRRLYLKGTGTAG-----KQSSLLHGADEFSTKDADNDNCMCAL 441
QY 295 LVNGQSVKSCSHLNKGTWMPNECGLANLINGIHFS-----GKLLATGIOMGTWKNNSPV 350
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   DB 485 SLRSTMMIR 494

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RESULT 7

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US-09-897-306-13
; Sequence 13, Application US/09897306
; Patent No. US20020123054A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Gorgone, Gina A.
; APPLICANT: Patterson, Chandra
; APPLICANT: Murty, Lynn E.
; TITLE OF INVENTION: HUMAN ANGIOPOIETIN
; FILE REFERENCE: PC-0048 CIP
; CURRENT APPLICATION NUMBER: US/09/897,306
; CURRENT FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020123054A1 g1907327
US-09-897-306-13

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Query Match 19.8%; Score 395; DB 10; Length 498;
Best Local Similarity 27.0%; Pred. No. 1.2e-29;
Matches 116; Conservative 66; Mismatches 126; Indels 122; Gaps 16;

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   DB 164 LENSLSYKLEKOLLQOTNEILKHEKNSLLEHKLLEMEGKHKELDPTLKEKENLOGLV 223
QY 83 DEQOASLDYLSNOVN-----ELM-----NRVLLLTVEF-----RKOLDPF 118
   DB 224 TRQTYIIIOELEKOLNRTATNNSVLOKQOELMDTVHNLVNLCTKEGVLLKGGKREEKPF 283
QY 119 PHRVOSHGLDCTDIKDTIGSVTKTPSGLYIIPREGSSYPFEVWCDMDYRGCGWTYIOKR 178
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QY 239 YDNFWLEDETRFEFKMLHGRISGNAGDAFRGLKEDN--QNAAMPSTSDVNDGCRPAC-- 294
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   DB 485 SLRSTMMIR 494

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RESULT 8

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US-09-998-831-5
; Sequence 5, Application US/09998831
; Patent No. US20020119153A1
; GENERAL INFORMATION:
; APPLICANT: Philip E. Thorpe
; APPLICANT: Rolf A. Brecken
; TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY
; FILE REFERENCE: 4001.002584
; CURRENT APPLICATION NUMBER: US/09/998,831
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 09/561,108
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-998-831-5

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Query Match 19.7%; Score 394; DB 10; Length 495;
Best Local Similarity 27.0%; Pred. No. 1.5e-29;
Matches 116; Conservative 66; Mismatches 126; Indels 122; Gaps 16;

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QY 63 LONSIYSV-----TRSTKLLRNM 82
   DB 161 LENSLSYKLEKOLLQOTNEILKHEKNSLLEHKLLEMEGKHKELDPTLKEKENLOGLV 220
QY 83 DEQOASLDYLSNOVN-----ELM-----NRVLLLTVEF-----RKOLDPF 118
   DB 221 TRQTYIIIOELEKOLNRTATNNSVLOKQOELMDTVHNLVNLCTKEGVLLKGGKREEKPF 280
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   DB 281 -----RDCADYV-----QAGFNKSGITYITYINNMPREKKYFCANDVGGCGWTYIOHR 327
QY 179 IDGIIDFORIMCDYLDGFGDLGFEWLGKFIYIVNOKNTSFMLYVALESEDPTLAYAS 238
   DB 328 EDGSLDFORGMKEKYMFGNPSGEYWLGNFEIFAITSOR--QYMLRIELMDWEGNRAYSQ 385
QY 239 YDNFWLEDETRFEFKMLHGRISGNAGDAFRGLKEDN--QNAAMPSTSDVNDGCRPAC-- 294
   DB 386 YDRFHIGNEKQNRRLYLKGTGTAG-----KQSSLLHGADEFSTKDADNDNCMCAL 438
QY 295 LVNGQSVKSCSHLNKGTWMPNECGLANLINGIHFS-----GKLLATGIOMGTWKNNSPV 350
   DB 439 MLTG-----GWMFDACGSPSNLNGMFTYTAQONHCKL--NQIKMHYF--KGPSY 481
QY 351 KIKSVSMKIR 360
   DB 485 SLRSTMMIR 494

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Db 176 QOFLVYCEIDSGNGWIVFQKRLDGSVDFKKNMIOYKEGFGHLSPTGTEFNLGNEKHL 235
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Qy 272 ED-----NONAMPFSTDVNDGCRPACLVNGOSVYKSCSHLNKKTGMWFNEGCLANL 323
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Db 345 NGVYYGGTYSKASTPNGYDNGIIMATW-----KTRWYSMK 380
RESULT 14
US-09-912-741B-1
; Sequence 1, Application US/09912741B
; Patent No. US20020131970A1
; GENERAL INFORMATION:
; APPLICANT: Allert, Dario C
; APPLICANT: Langulino, Lucia R
; APPLICANT: Thornton, George B
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING
; TITLE OF INVENTION: ENDOTHELIAL CELL AND FIBRINOGEN MEDIATED INFLAMMATION
; FILE REFERENCE: 300.1D1V4
; CURRENT APPLICATION NUMBER: US/09/912,741B
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: US 09/347,877
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 08/748,150
; PRIOR FILING DATE: 1996-11-12
; PRIOR APPLICATION NUMBER: US 08/232,532
; PRIOR FILING DATE: 1994-04-25
; PRIOR APPLICATION NUMBER: US 08/139,562
; PRIOR FILING DATE: 1993-10-19
; PRIOR APPLICATION NUMBER: US 07/898,117
; PRIOR FILING DATE: 1992-06-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: expressed
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: 88
; OTHER INFORMATION: site of glycosylation
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (153)...(182)
; OTHER INFORMATION: disulfide-bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (326)...(339)
; OTHER INFORMATION: disulfide-bond
US-09-912-741B-1
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Best Local Similarity 27.5%; Pred. No. 2e-26;
Matches 111; Conservative 52; Mismatches 136; Indels 102; Gaps 15;
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Qy 104 LLTTEVFRKQLDPPRHP-----VQSH--GLDCTDIKDTISVTKTSGLTIHPSS 156

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RESULT 15
US-09-992-598-314
; Sequence 314, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerder, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106

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55	PRIOR APPLICATION NUMBER: 60/091544
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58	PRIOR FILING DATE: 1998-07-02
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62	PRIOR FILING DATE: 1998-07-02
63	PRIOR APPLICATION NUMBER: 60/091978
64	PRIOR FILING DATE: 1998-07-07
65	PRIOR APPLICATION NUMBER: 60/091982

